ALLELE	STANDARD	SEQUENCE	SEQ ID NO:	BINDING
	PEPTIDE			AFFINITY
				(nM)
A*0101	944.02	YLEPAIAKY	3475	25
A*0201	941.01	FLPSDYFPSV	3476	5.0
A*0202	941.01	FLPSDYFPSV	3476	4.3
A*0203	941.01	FLPSDYFPSV	3476	10
A*0206	941.01	FLPSDYFPSV	3476	3.7
A*0207	941.01	FLPSDYFPSV	3476	23
A*6802	1141.02	FTQAGYPAL	3477	40
A*0301	941.12	KVFPYALINK	3478	11
A*1101	940.06	AVDLYHFLK	3479	6.0
A*3101	941.12	KVFPYALINK	3478	18
A*3301	1083.02	STLPETYVVRR	3480	29
A*6801	941.12	KVFPYALINK	3479	8.0
A*2402	979.02	AYIDNYNKF	3481	12
B*0702	1075.23	APRTLVYLL	3482	5.5
B*3501	1021.05	FPFKYAAAF	3483	7.2
B51	1021.05	FPFKYAAAF	3483	5.5
B*5301	1021.05	FPFKYAAAF	3483	9.3
B*5401	1021.05	FPFKYAAAF	3483	10

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le V. HLA Class II Standard Peptide Binding Affinity.

					<u>~</u> -
Allele	Nomenclature	Standard	Sequence	SEQ ID	Bigging
		Peptide		NO:	Affinity
					(nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	3484	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	3485	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	3484	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	3486	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	3486	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	3487 ,	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	3487	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	3487	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	3487	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	3487	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	3488	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3489	3.5
DRB1*1501	DR2w2β1	507.02	GRTQDENPVVHFFKNI	3490	9.1
			VTPRTPPP		
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	3491	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	3486	58
DRB5*0101	DR2w2β2	553.01	QYIKANSKFIGITE	3487	20
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The "Nomenclature" column lists the allelic designations used in Tables XIX and XX. SF 1094066 v1

Conserva	ancy	Freq.	Protein	Position	Sequence	SEQ ID NO:	String	A*0101
	95	. 19	POL	521	AICSVVRRAF	1 .	XIXXXXXXXF	
	95	19	NUC	54	ALRQAILÇW	2	XLXXXXXXXW	
	80	16	₽W	108	AMOWNSTTF	3	XMXXXXXXF	
	100 100	20 20	POL POL	166 166	ASFCGSPY	4 . 5	XSXXXXXY XSXXXXXXXW	
	90	18	NUC	19	ASFCGSPYSW ASKLCLGW	6	xsxxxxx	
	85	17	NUC	19	ASKLCLGWLW	7	xsxxxxxxx	
	80	16	POL.	822	ASPLHVAW	8 9	XSXXXXXW	•
	100 100	20 20	BW BW	312 312	CIPIPSSW CIPIPSSWAF	10	XIXXXXXW XIXXXXXXXF	
	95	19	₽₩	253	CLIFLLVLLDY	11	XLXXXXXXXXX	
	95	19	BW	239	CLRRFIIF	12	XLXXXXXF	
	75 95	15 19	ENV POL	239 523	CLRRFIIFLF	13 14	XLXXXXXXXF XSXXXXXF	
•	100	20	BW BW	310	CSVVRRAF CTCIPIPSSW	15	XTXXXXXXXX	
	90	18	NUC	31	DIDPYKEF	16	XIXXXXXF	44.4000
	85 95	17 19	NUC BW	29 196	DLLDTASALY	17 18	XLXXXXXXXY XSXXXXXXF	11.1000
	95	19	NC	43	OSWWTSLNF ELLSFLPSDF	19	XLXXXXXXXF	•
	95	19	NUC -	43	ELLSFLPSDFF	20	XLXXXXXXXXX	
	95 95	19	POL	374	ESRLVVDF	21	XSXXXXXF XSXXXXXXXXF	
	80	19 16	POL ENV	374 248	ESRLVVDFSQF FILLLCLIF	22 23	XIXXXXXXF	
	80	16	BW.	246	FLFILLLCLIF	24	XLXXXXXXXXF	
	95	19	BW	256	FLLVLLDY	25	XDXXXXX	
	95 90	19 18	POL X	658 63	FSPTYKAF FSSAGPCALRF	26 27	XSXXXXXF XSXXXXXXXXF	
	100	20	₽Ŵ	333	FSWLSLLVPF	28	XSXXXXXXX	
	95	19	, POL	656	FTFSPTYKAF	29	XTXXXXXXXF	
	95 95	19 19	EW POL	346 627	FVGLSPTVW	30 31	XVXXXXXXXW XLXXXXXXF	
	95	19	POL POL	509	GLLGFAAPF GLSPFLLAQF	32	XLXXXXXXXF	
	85	17	NUC	29	GMDIDPYKEF	33	XMXXXXXXF	
	95 75	19	NUC 800	123	GVWIRTPPAY	34	XVXXXXXXXY	0.0017
	80	15 16	POL POL	569 491	HLNPNKTKRW HLYSHPIILGF	35 36	XLXXXXXXXW XLXXXXXXXXF	
	85	17	POL	715	HTAELLAACF	37	XTXXXXXXF	
	95	19	NUC	52	HTALRQAILCW	38	XTXXXXXXXXW	0.0300
	100 100	20 20	POL BW	149 249	HTLWKAGILY ILLLCLIF	39 40	XTXXXXXXXY XLXXXXXF	0.0300
	80	16	POL	760	ILRGTSFVY	41	XLXXXXXXY	0.0017
	90	18	₽W	188	ILTIPOSLDSW	42	XLXXXXXXXXX	
	90 80	18 16	POL POL	625 503	IVGLLGFAAPF KIPMGVGLSPF	43 44	XVXXXXXXXF	
	85	17	NUC	21	KLCLGWLW	45	XLXXXXXW	
	75	15	POL	108	KLIMPARF	46	XLXXXXXF	0.0047
	75 80	15 16	POL POL	108 610	KLIMPARFY	47 48	XLXXXXXXY	0.0017
	85	17	POL.	574	KLPVNRPIDW KTKRWGYSLNF	49	XTXXXXXXXF	
	95	19	POL	55	KVGNFTGLY	50	XVXXXXXXY	0.0680
	95 100	19 20	EW POL	254 109	LIFLLVLLDY	5 1 5 2	XIXXXXXXY	0.0084
	85	17	NUC	30	LIMPARFY LLDTASALY	53	XLXXXXXXY	25.0000
	80	16	POL	752	LLGCAANW	54	XLXXXXXW	
	95 100	19	POL.	628	LLGFAAPF	55 56 ·	XLXXXXXF XLXXXXXXW	
	100	20 20	<b>8</b> ₩	378 378	LLPIFFCLW	57	XLXXXXXXXX .	•
	95	19	NUC	44	LLSFLPSDF	58	XLXXXXXXF	
	95	19	NUC	44	LLSFLPSDFF	59	XLXXXXXXXF	
	90 95	18 19	POL BW	407 175	LLSSNLSW LLVLQAGF	60 61	XLXXXXXW XLXXXXXF	
	95	19	₽W	175	LLVLQAGFF	62	XLXXXXXXF	
	100	20	BW.	338	LLVPFVQW	63	XLXXXXXW	
	100 85	20 17	NUC NUC	338 100	LLVPFVQWF LLWFHISCLTF	64 65	XLXXXXXXF XLXXXXXXXXF	
	95	19	NUC	45	LSFLPSDF	66	XSXXXXXF	
	95	19	NUC	45	LSFLPSDFF	67	XSXXXXXXF	
	95 95	19 19	POL POL	415 415	LSLDVSAAF LSLDVSAAFY	68 69	XSXXXXXXF XSXXXXXXXY	4.2000
•	100	20	BW	336	LSLLVPFVQW	70	xsxxxxxxx	
	100	20	₽W	336	LSLLVPFVQWF	71	XSXXXXXXXXF	
	95 95	19	×	53	LSLRGLPVCAF	72 73	XSXXXXXXXF XSXXXXXXF	
	75	19 15	POL BW	510 349	LSPFLLAGF LSPTVWLSVIW	73 74	XSXXXXXXXX	
	85	17	POL	742	LSRKYTSF	75	XSXXXXXF	
	85	17	POL.	742	LSRKYTSFPW	, 76 , 77	XSXXXXXXXW	
	75 75	15 15	NUC BW	16 137	LSVPNPLGF LTFGRETVLEY	, 77 78	XSXXXXXXF XTXXXXXXXXY	
	90	18	BW	189	LTIPOSLDSW	79	XTXXXXXXXX	
	90	18	BW.	189	LTIPOSLDSWW	80	XTXXXXXXXXW	
	90 95	18	POL BM	404 176	LTNLLSSNLSW	8 1 8 2	XTXXXXXXXXW XVXXXXXXF	
	100	19 20	. BW BW	176 339	LVLQAGFF LVPFVQWF	83	XVXXXXXF	
	100	20	POL	377	LVVDFSQF	84	XVXXXXXF	
	85 75	17 15	EW X	360 103	MMWYWGPSLY	85 86	XMXXXXXXXY XSXXXXXXY	0.0810 0.8500
	75	15	×	103	MSTTDLEAY MSTTDLEAYF	86 87	XSXXXXXXXF	5.5500
		-	**			- ·	-	

95 19 PCL 42 NLGNLNVSIPW 88 XLXXXXXXXVY 90 18 PCL 406 NLLSSNLSW 89 XLXXXXXXXVY 95 19 PCL 45 NLNVSIPW 90 XLXXXXXXXV 75 15 BW 15 NLSVPNPLGF 91 XLXXXXXXXXF 90 18 PCL 738 NSVVLSRKY 92 XSXXXXXXXY 100 20 BW 380 PIFFCLWVY 93 XIXXXXXXXY	
90 18 POL 406 NLLSSNLSW 89 XLXXXXXXW 95 19 POL 45 NLNVSIPW 90 XLXXXXXXW 75 15 BNV 15 NLSVPNPLGF 91 XLXXXXXXXF 90 18 POL 738 NSVVLSRKY 92 XSXXXXXXY	
95 19 POL 45 NLNVSIPW 90 XLXXXXXXV 75 15 BNV 15 NLSVPNPLGF 91 XLXXXXXXXF 90 18 POL 738 NSVVLSRKY 92 XSXXXXXXY	
90 18 POL 738 NSV/LSRKY 92 XSXXXXXXY	
100 20 ENV 380 PIFFCLWYY 93 XIXXXXXXY	0.0005
	0.0078
100 20 EW 314 PIPSSWAF 94 XIXXXXXF	
100 20 POL 124 PLDKGIKPY 95 XLXXXXXXY	0.0190
100 20 POL 124 PLDKGIKPYY 96 XLXXXXXXY	0.1600
100 20 EW 377 PLIPIFFCLW 97 XIXXXXXXX	
95 19 BW 174 PLLVLQAGF 98 XLXXXXXXF	
95 19 BW 174 PLIVLQAGFF 99 XLXXXXXXXF	
80 16 POL 505 PMGVGLSPF 100 XMXXXXXXF 85 17 POL 797 PTTGRTSLY 101 XTXXXXXXY	0.7700
, Transcr	0.7700
95 19 POL 685 QVFADATPTG 104 XVXXXXXXXW 90 18 POL 624 RIVGLLGF 105 XIXXXXXF	
75 15 POL 106 RIKLIMPARF 106 XILXXXXXXXF	
75 15 POL 106 RIKLIMPARFY 107 XLXXXXXXXXY .	
95 19 POL 376 RLWOFSOF 108 XLXXXXXXF	
90 18 POL 353 RTPARVTGGVF 109 XTXXXXXXXF	
100 20 POL 49 SIPWTHKYGNF 110 XIXXXXXXXXF	
95 19 BNV 194 SLDSWVTSLNF 111 XLXXXXXXXXF	
95 19 POL 416 SLDVSAAF 112 XLXXXXXF	
95 19 POL 416 SLDVSAAFY 113 XLXXXXXXY	17.2000
100 20 ENV 337 SLLVPFVQW 114 XLXXXXXXW	
100 20 EW 337 SLLVPFVQWF 115 XLXXXXXXXF	
95 19 X 54 SLRGLPVCAF 116 XLXXXXXXXF	
90 18 X 64 SSAGPCALRF 117 XSXXXXXXF	
75 15 X 104 STTDLEAY 118 XTXXXXXY	
75 15 X 104 STTDLEAYF 119 XTXXXXXF	
75 15 EW 17 SVPNPLGF 120 XVXXXXXF 90 18 POL 739 SVVI SRKY 121 XVXXXXXY	
OTTEORITE TO THE PROPERTY OF T	
90 18 EW 190 TIPQSLDSW 123 XIXXXXXXW 90 18 EW 190 TIPQSLDSWW 124 XIXXXXXXXW	
100 20 POL 150 TLWKAGILY 125 XLXXXXXXY	0.0017
75 15 X 105 TTDLEAYF 126 XTXXXXXF	
85 17 POL 798 TTGRTSLY 127 XTXXXXXY	•
80 16 NC 16 TVQASKLCLGW 128 XVXXXXXXXW	
75 15 EW 352 TVWLSVIW 129 XVXXXXXW	
85 17 POL 741 VLSRKYTSF 130 XLXXXXXXF	
85 17 POL 741 VLSRKYTSFPW 131 XLXXXXXXXV	
85 17 POL 740 VVLSRKYTSF 132 XVXXXXXXF	
80 16 POL 759 WILRGTSF 133 XIXXXXXF	
80 16 POL 759 WILRGTSFVY 134 XIXXXXXXY	0.0023
95 19 NUC 125 WIRTPPAY 135 XIXXXXXY	
80 16 POL 751 WLLGCAANW 136 XLXXXXXXW 95 19 POL 414 WLSLDVSAAF 137 XLXXXXXXF	
TO COLUMN TO THE TAXABLE PARTY OF TAXABLE	
100 20 EW 335 WLSLLVPF 139 XLXXXXXXF 100 20 EW 335 WLSLLVPFVQW 140 XLXXXXXXXXW	
85 17 NuC 26 W.WGMDIDPY 141 XLXXXXXXXY	0.0810
95 19 ENV 237 WMCLRRFIIF 142 XMXXXXXXF	
85 17 ENV 359 WMMWYYWGPS 143 XMXXXXXXXY	
100 20 POL 52 WTHKVGNF 144 XTXXXXXF	
100 20 POL 122 YLPLDKGIKPY 145 XLXXXXXXXY	
90 18 NUC 118 YLVSFGVW 146 XLXXXXXW	
80 16 POL 493 YSHPIILGF 147 XSXXXXXF	
85 17 POL 580 YSLNFMGY 148 XSXXXXXY	

SECID   A.C.   A.C.	Table VIII				HBV A02 SUP	ER MOTIF	SUPER MOTIF (With binding information	informa	tion)			
17   POL   721   AACFARSRSCA   149   11	rvancy Fr		Protein	Position	Sequence	SEQ ID NO:	AA.	A.0201	A*0202	A.0203	A.0206	A.6802
17   P.C.   431   AAMPHLLV   150   151	r.	17	8	721	AACFABSBSGA	149	11					
16   POL   756   AAMWILROT   151	· ю	17	<u>ද</u>	431	AAMPHLLV	150	΄ ω				٠	
19   POL   632   AAPFTOCGYPA   152   11	0	16	점	756	AANWILRGT	151	6					
19   PCL   S21   ALCSWURPA   153   9   0.0001     18   NLC   58   ALCWGEM   155   9   0.0001     19   PCL   642   AMPILYACI   156   9   0.5000     10   AMOWINSTT   157   9   0.0013     11   PCL   516   AMPTROLEA   158   9   0.0013     12   PCL   516   AMPTROLEA   158   9   0.0013     13   PCL   516   AMPTROLEA   161   8   10     14   PCL   516   AMPTROLEA   162   9   0.0013     15   PCL   510   AMPTROLEA   162   9   0.0001     16   PCL   530   AMPTROLEA   164   8   0.0001     17   PCL   530   AMPRICAL   165   9   0.0001     18   PCL   530   AMPRICAL   165   9   0.0001     19   X   61   CAFSAGPCA   168   11   0.0001     10   X   61   CAFSAGPCA   168   11   0.0001     11   PCL   533   CAFSWIDDY   177   10   0.0001     12   RCL   533   CAFSWIDDY   177   18   0.0001     13   RCL   533   CAFSWIDDY   177   18   0.0001     14   RCL   533   CAFSWIDDY   177   18   0.0001     15   BW   233   CAFSWIDDY   177   18   0.0001     16   X   7   CALIFILL   178   9   0.0001     17   RUC   23   CARWINGM   178   9   0.0001     18   RCL   533   CAFSWIDDY   178   9   0.0001     19   RCL   533   CAFSWIDDY   178   9   0.0001     10   RUC   107   CATFGETY   181   18   18   19     11   RUC   107   CATFGETY   181   18   18   19     12   RCL   622   CARVINGH   184   10   11     13   RCL   622   CARVINGH   187   18   19     14   RCL   622   CARVINGH   187   19   19     15   RCL   682   CARVINGH   187   18   19     15   RCL   684   CAFRATH   180   10   10   10     15   RCL   684   CAFRATH   180   10   10   10     16   RCL   684   CAFRATH   180   10   10   10     18   RCL   684   CAFRATH   190   9   0.0001     19   RCL   685   CARVINGH   190   9   0.0001     10   RCL   685   CARVINGH   190   9   0.0001     11   RCL   685   CARVINGH   190   9   0.0001     12   RCL   685   CARVINGH   190   9   0.0001     13   RCL   685   CARVINGH   190   9   0.0001     14   RCL   685   CARVINGH   190   9   0.0001     15   RCL   685   CARVINGH   190   9   0.0001     15   RCL   685   CARVINGH   190   9   0.0001     15   RCL   685   CARVINGH   190   9   0.0001	2	19	절	632	AAPFTGCGYPA	152	=		,			
18	2	19	젙	521	AICSVVRRA	153	6	0.0001				
18         NLC         5.8         ALICWGELM         155         9         0.5000           16         BAN         642         ALIMPLYACI         156         9         0.5000           16         BAN         ALIMPLYACI         156         9         0.5000           15         X         102         AMSTDLEA         158         9         0.0013           19         POL         516         AOPTSAICSV         160         11         0.0013           19         POL         516         AOPTGAICSV         160         11         0.0013           19         POL         690         APPTGWGLA         161         8         0.0001           19         POL         690         APPTGWGLA         162         9         0.0001           19         POL         690         APPTGWGLA         162         9         0.0001           19         POL         397         APPLICASIT         165         9         0.0001           19         POL         397         APPLICASIT         165         9         0.0001           19         POL         397         APPLICASIT         165         0.0001	0	8	3	28	AILCWGEL	154	&					
19   POL   642   ALMPUYACI   156   9   0.5000     15   X	0	18	3	58	AILCWGELM	155	6					
16   BW   108   AMCMNISTT   157   8   19   PQL   216   AMFTROLEA   158   9   10   119   PQL   516   AMFTROLEA   158   9   10   119   PQL   516   AMFTROLEA   159   10   119   PQL   516   AMFTROLEA   161	2	19	젍	642	ALMPLYACI	156	o	0.5000	0.0340	3.3000	0.2500	0.0470
15         X         102         AMSTTDLEA         158         9           19         POL         516         AOFTSANCSV         159         10           19         POL         516         AOFTSANCSV         160         11           19         POL         516         AOFTSANCSV         160         11           16         POL         690         ATPTGWGLAI         161         8           19         POL         397         AVPNLOSLT         163         10           19         POL         397         AVPNLOSLTNI         164         8           19         POL         397         AVPNLOSLTNI         165         9           19         X         61         CAFSSAGPCA         169         11           10         X         61         CALFSTMDDV         173         11           10         X         69         CALFSTMDDV <t< td=""><td>0</td><td>16</td><td><b>8</b></td><td>108</td><td>AMOWNSTT</td><td>157</td><td>œ</td><td></td><td></td><td></td><td></td><td>•</td></t<>	0	16	<b>8</b>	108	AMOWNSTT	157	œ					•
19         POL         516         AQFTSACSV         159         10           19         POL         516         AQFTSACSVY         160         11           19         POL         690         ATPTGWGLA         161         8           15         POL         690         ATPTGWGLA         162         9           19         POL         690         ATPTGWGLA         162         9           19         POL         397         AVPNLOSLTH         166         11           19         POL         540         CALRFTSA         167         10           10         X         61         CAESSAGPCA         177         11           10         X         61         CALRFTSA         177         11           10         X         533         CLAFSYMDDV         17	S.		×	102	AMSTTDLEA	158	6	0.0013				
19         POL         516         AQFTSAICSVV         160         11           19         POL         690         ATPTGWGLA         162         9           16         POL         690         ATPTGWGLA         162         9           19         POL         397         AVPNLOSLT         164         8           19         POL         397         AVPNLOSLT         164         8           19         POL         397         AVPNLOSLT         164         8           19         POL         397         AVPNLOSLT         165         11           19         POL         397         AVPNLOSLT         166         11           19         POL         397         AVPNLOSLT         166         11           19         X         61         CAFSSAGPCA         166         11           19         X         61         CAFSSAGPCAL         168         10           10         X         61         CAFSSAGPCAL         168         11           10         X         61         CAFSSAGPCAL         168         10           10         X         61         CAFSSAGPCAL         168 <td>S.</td> <td>19</td> <td>젙</td> <td>516</td> <td>AQFTSAICSV</td> <td>159</td> <td>10</td> <td></td> <td></td> <td></td> <td></td> <td></td>	S.	19	젙	516	AQFTSAICSV	159	10					
19         POL         690         ATPTGWGL         161         8           16         POL         690         ATPTGWGLAI         162         9           15         POL         397         AVPNLOSL         16         9           19         POL         397         AVPNLOSL         16         11           19         POL         397         AVPNLOSL         165         9           19         POL         397         AVPNLOSL         165         11           16         POL         397         AVPNLOSL         166         11           19         X         61         CASSAGPCAL         166         10           19         X         61         CASSAGPCAL         168         10           19         X         61         CASSAGPCAL         168         10           18         X         61         CASSAGPCAL         168         10           18         X         61         CAFSYMDDV         177         8           19         POL         533         CLAFSYMDDV         175         8           10         BN         23         CLAFSYMDDV         174	LC L	<del>1</del> 9	전	516	AQFTSAICSVV	160	11					
16         POL         690         ATPTGWGLA         162         9           15         POL         690         ATPTGWGLAI         163         10           19         POL         397         AVPNLOSLT         164         8           19         POL         397         AVPNLOSLT         165         9           19         POL         397         AVPNLOSLT         166         11           16         POL         755         CAANWILGST         167         10           19         X         61         CAFSSAGPCAL         168         11           18         X         69         CALRTSA         170         8           20         BW         312         CIPPSSWA         171         9           16         BW         312         CIPPSSWARA         172         11           18         X         69         CALRFTSA         173         10           18         X         69         CALRFTSA         173         11           18         NOC         533         CLGAFSWADDW         174         11           17         NUC         23         CLGAMWGMD         174		19	절	069	ATPTGWGL	161	80					
15         POL         690         APPTGWGLAI         163         10           19         POL         397         AVPNLOSLT         164         8           19         POL         397         AVPNLOSLT         164         8           19         POL         397         AVPNLOSLT         165         11           16         POL         357         AVPNLOSLTNL         166         11           19         X         61         CAFSSAGPCAL         168         10           19         X         61         CAFSSAGPCAL         169         11           20         BW         312         CAFRFTSA         170         8           20         BW         312         CAFRFTSA         171         9           16         BW         312         CAFSWADDV         173         10           18         POL         533         CLAFSYMDDV         174         11           17         NAC         23         CLGMWGMDI         175         8           17         NAC         23         CLGMWGMDI         175         8           18         POL         533         CLGRWLWGM         176	0	16	절	069	ATPTGWGLA	162	o					
19         PQL         397         AVPNLQSLT         164         8           19         PQL         397         AVPNLQSLT         165         9           19         PQL         397         AVPNLQSLTNL         165         11           16         PQL         755         CAAPINIQST         166         11           19         X         61         CAFSSAGPCAL         168         10           19         X         61         CAFSSAGPCAL         169         11           10         X         61         CAFSSAGPCAL         169         11           10         X         61         CAFSSAGPCAL         168         10           10         X         61         CAFSSAGPCAL         168         11           10         X         61         CAFSSAGPCAL         168         11           10         X         61         CAFSSAGPCAL         168         10           11         X         61         CAFSSAGPCAL         168         11           11         BW         23         CAFSYMDDVA         172         11           12         BW         253         CLARLANCAL         175 </td <td>10</td> <td>15</td> <td>절</td> <td>069</td> <td>ATPTGWGLAI</td> <td>163</td> <td>10</td> <td></td> <td></td> <td></td> <td></td> <td></td>	10	15	절	069	ATPTGWGLAI	163	10					
19         POL         397         AVPNLQSLT         165         9           19         POL         755         CAANWILGSLTNL         166         11           16         POL         755         CAANMILGSLTNL         166         11           19         X         61         CAFSSAGPCAL         168         10           19         X         61         CAFSSAGPCAL         169         11           18         X         69         CALRFTSA         170         8           20         BW         312         CIPPSSWAFA         171         9           16         BW         312         CIPPSSWAFA         172         11           18         POL         533         CLAFSYMDDV         174         11           17         NUC         23         CLAFSYMDDV         175         8           20         BW         253         CLAFLVL         177         8           20         BW         253         CLIFLLVL         177         8           19         BW         253         CLIFLLVL         178         9           15         BW         253         CLIFLLVL         178		19	ಕ	397	AVPNLOSL	164	80					
19         POL         397         AVPNLQSLTNL         166         11           16         POL         755         CAANWILRGT         167         10           19         X         61         CAFSSAGPCA         168         10           19         X         61         CAFSSAGPCAL         169         11           18         X         69         CALRFTSA         170         8           20         BNV         312         CIPIPSSWAFA         171         9           16         BNV         312         CIPIPSSWAFA         172         11           18         POL         533         CLAFSYMDDV         173         10           17         NLC         23         CLGWLWGMM         174         11           20         BW         253         CLGNLWGMM         176         10           20         BW         253         CLGRLLVL         177         8           19         BW         253         CLRFIFIC         177         8           19         BW         239         CLRFIFIC         179         9           16         X         7         CQLDPABADY         182	10	19	젍	397	AVPNLOSLT	165	6	0.0001				
16         PQL         755         CAANWILRGT         167         10           19         X         61         CAFSSAGPCAL         168         10           19         X         61         CAFSSAGPCAL         168         10           18         X         61         CAFSSAGPCAL         168         11           20         BW         312         CIPPTSAM         170         8           16         BW         312         CIPPTSSWAPA         173         10           18         POL         533         CLAFSYMDDV         173         10           18         POL         533         CLAFSYMDDV         174         11           17         NUC         23         CLAFSYMDDV         174         11           17         NUC         23         CLAFLVIL         175         8           17         NUC         23         CLIFLLVIL         176         9           19         BW         253         CLIFLLVIL         178         9           18         NUC         107         CLIFGRETY         181         8           16         X         7         CQLDPARDY         183		19	젙	397	AVPNLOSLTNL	166	Ξ					
19         X         61         CAFSSAGPCA         168         10           19         X         61         CAFSSAGPCAL         169         11           18         X         69         CALRFISA         170         8           20         BAV         312         CIPIPSSWAFA         172         11           16         BAV         312         CIPIPSSWAFA         172         11           18         POL         533         CLGFSYMDDV         174         11           17         NAC         23         CLGMLWGMDI         176         10           20         BW         253         CLGTLVL         177         8           20         BW         253         CLIFLLVL         178         9           20         BW         253         CLRENIFLE         179         9           19         BW         239         CLRRFIIFL         179         9           15         BW         239         CLRGRFIT         181         8           16         X         7         COLDPABDY         183         9           16         X         7         COLDPABDY         184         10	_	16	젍	755	CAANWILRGT	167	10					
19         X         61         CAFSSAGPCAL         169         11           20         BNV         312         CIPIPSSWA         171         9           16         BNV         312         CIPIPSSWAFA         172         11           16         BNV         312         CIPIPSSWAFA         172         11           18         POL         533         CLAFSYMDDV         173         10           18         POL         533         CLAFSYMDDV         174         11           17         NUC         23         CLGRWWGMDI         176         10           20         BNV         253         CLIFLLVL         177         8           20         BNV         253         CLIFLLVL         178         9           20         BNV         253         CLIFLLVL         178         9           15         BNV         239         CLRRFIIFLF         179         9           16         X         7         CQLPARDAT         181         8           16         X         7         CQLPARDAT         184         10           19         POL         684         CQVFADAT         189	10	19	×	61	CAFSSAGPCA	168	10	0.0001				
18         X         69         CALRFTSA         170         8           20         BN         312         CIPIPSSWA         171         9           16         BN         312         CIPIPSSWAFA         172         11           18         POL         533         CLAFSYMDDV         173         10           18         POL         533         CLAFSYMDDV         174         11           17         NUC         23         CLGMLWGMDI         175         8           20         BN         253         CLGRLVL         177         8           20         BN         253         CLFLVL         177         8           20         BN         253         CLFLVL         177         8           15         BN         239         CLFRILLYL         177         8           16         NLC         107         CLFGRETY         181         9           16         NL         107         CLFGRETY         181         10           16         X         7         CQLDPARDY         184         10           17         POL         622         CQRIVGLL         18         11		19	×	61	CAFSSAGPCAL	169	=					
20         BNV         312         CIPIPSSWA         171         9           16         BNV         312         CIPIPSSWAFA         172         11           18         POL         533         CLAFSYMDDVV         173         10           17         NLC         23         CLAFSYMDDVV         175         8           17         NLC         23         CLGMLWGMDI         176         10           20         BNV         253         CLIFLLVL         177         8           20         BNV         253         CLRFIIFL         178         9           15         BN         239         CLRFIIFL         179         9           16         NLC         107         CLTGRFIT         181         8           16         NLC         107         CLTGRFIT         182         9           16         X         7         CQLDPARDV         183         9           16         X         7         CQLDPARDV         185         8           17         POL         622         CQRIVGLGA         16         10           19         POL         684         CQVFADATPT         190	_	8	×	69	CALRFTSA	170	80					
16         BW         312         CIPIPSSWAFA         172         11           18         POL         533         CLAFSYMDDV         173         10           18         POL         533         CLAFSYMDDV         174         11           17         NUC         23         CLGWLWGMDI         176         10           20         BW         253         CLIFLUL         177         8           20         BW         253         CLIFLULL         178         9           19         BW         239         CLRRFIIFL         179         9           15         BW         239         CLRRFIIFL         180         11           18         NUC         107         CLTFGRET         181         8           18         NUC         107         CLTFGRETY         182         9           16         X         7         CQLDPARDV         183         9           16         X         7         CQLDPARDV         184         10           17         POL         622         CQRIVGLL         185         8           17         POL         684         CQVFADAT         189 <t< td=""><td>0</td><td>50</td><td><b>≥</b></td><td>312</td><td>CIPIPSSWA</td><td>171</td><td>o</td><td>0.0010</td><td></td><td></td><td></td><td></td></t<>	0	50	<b>≥</b>	312	CIPIPSSWA	171	o	0.0010				
18         POL         533         CLAFSYMDDV         173         10           18         POL         533         CLAFSYMDDVV         174         11           17         NUC         23         CLGMLWGMDI         176         10           20         BNV         253         CLIFLLVL         177         8           20         BNV         253         CLIFLLVL         178         9           19         BNV         239         CLRRFIIFL         179         9           15         BNV         239         CLRRFIIFL         180         11           18         NUC         107         CLTFGRET         181         8           18         NUC         107         CLTFGRETY         182         9           16         X         7         CQLDPARDV         183         9           16         X         7         CQLDPARDV         184         10           17         POL         622         CQRIVGLL         185         8           17         POL         684         CQVFADAT         189         11           19         POL         684         CQVFADAT         190	_	16	2	312	CIPIPSSWAFA	172	=					
18         POL         533         CLAFSYMDDVV         174         11           17         NUC         23         CLGMLWGM         175         8           17         NUC         23         CLGMLWGMDI         176         10           20         BNV         253         CLIFLLVL         177         8           20         BNV         239         CLRRFIIFL         179         9           15         BNV         239         CLRRFIIFL         180         11           18         NUC         107         CLTFGRET         181         8           18         NUC         107         CLTFGRET         181         8           16         X         7         CQLDPARDV         183         9           16         X         7         CQLDPARDV         184         10           17         POL         622         CQRVGLL         185         8           17         POL         684         CQVFADAT         187         8           19         POL         684         CQVFADAT         190         9           20         BNV         310         CTCIPIPSWA         189 <td< td=""><td>_</td><td>18</td><td>전</td><td>533</td><td>CLAFSYMDDV</td><td>173</td><td>10</td><td>0.0008</td><td></td><td></td><td></td><td></td></td<>	_	18	전	533	CLAFSYMDDV	173	10	0.0008				
17         NUC         23         CLGMLWGMD         175         8           17         NUC         23         CLGMLWGMDI         176         10           20         BNV         253         CLIFLULL         177         8           20         BNV         239         CLRRFIIFL         179         9           15         BNV         239         CLRRFIIFLFI         180         11           18         NUC         107         CLTFGRET         181         8           18         NUC         107         CLTFGRETY         182         9           16         X         7         CQLDPARDV         183         9           16         X         7         CQLDPARDVL         184         10           17         POL         622         CQRNGLL         185         8           17         POL         622         CQRNGLGLGFA         186         11           19         POL         684         CQVFADAT         189         11           20         BNV         310         CTCIPIPSSWA         189         11           20         BNV         310         CTCIPIPSGLGL         190	_	18		533	CLAFSYMDDVV	174	7					
17         NUC         2.3         CLGWLWGMDI         176         10           20         BNV         25.3         CLIFLUL         177         8           20         BNV         25.3         CLRAFIFL         179         9           19         BNV         239         CLRAFIFLFI         180         11           18         NJC         107         CLTFGRET         181         8           18         NJC         107         CLTFGRETY         182         9           16         X         7         CQLDPARDV         183         9           16         X         7         CQLDPARDVL         184         10           17         POL         622         CQRNGLL         185         8           17         POL         622         CQRNGLGFA         186         11           19         POL         684         CQVFADAT         187         8           20         BNV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9		17	3	23	CLGMLWGM	175	æ					
20         BW         253         CLIFLUL         177         8           20         BW         253         CLIFLULL         178         9           19         BW         239         CLRRFIIFL         179         9           15         BW         239         CLRRFIIFL         180         11           18         NJC         107         CLTFGRET         181         8           16         X         7         CQLDPARDV         183         9           16         X         7         CQLDPARDVL         184         10           17         POL         622         CQRVGLL         185         8           17         POL         622         CQRVGLL         185         8           17         POL         684         CQVFADAT         187         8           19         POL         684         CQVFADATPT         189         11           20         BNV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9		17	3	23	CLGWLWGMDI	176	10	0.0093				
20         BNV         253         CLIFLULL         178         9           19         BNV         239         CLRRFIIFL         179         9           15         BNV         239         CLRRFIIFLF1         180         11           18         NUC         107         CLTFGRET         181         8           18         NUC         107         CLTFGRETY         182         9           16         X         7         CQLDPARDY         183         9           16         X         7         CQLDPARDYL         184         10           17         POL         622         CQRNGLL         185         8           17         POL         622         CQRNGLGFA         186         11           19         POL         684         CQVFADAT         187         8           20         BNV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9	0	20	2	253	CLIFLLYL	177	80	0.0002				
19         BNV         239         CLRRFIIFL         179         9           15         BNV         239         CLRRFIIFLFI         180         11           18         NJC         107         CLTFGRETY         181         8           16         X         7         CQLDPARDY         183         9           16         X         7         CQLDPARDYL         184         10           17         POL         622         CQRIVGIL         185         8           17         POL         622         CQRIVGILGFA         186         11           19         POL         684         CQVFADAT         187         8           20         BNV         310         CTCIPIPSSWA         189         11           20         BNV         310         CTCIPIPSSWA         190         9	0	20	3	253	CLIFLYLL	178	თ	9000.0				
15         BNV         239         CLRRFIIFLFI         180         11           18         NUC         107         CLTFGRET         181         8           18         NUC         107         CLTFGRETY         182         9           16         X         7         CQLDPARDVL         183         9           16         X         7         CQLDPARDVL         184         10           17         POL         622         CQRIVGLL         185         8           17         POL         682         CQRIVGLLGFA         186         11           19         POL         684         CQVFADAT         187         8           19         POL         684         CQVFADATPT         188         10           20         BNV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9	٠.	19	2	239	CLRRFIIFL	179	6	0.0002				
18         NUC         107         CLTFGRET         181         8           18         NUC         107         CLTFGRETY         182         9           16         X         7         CQLDPARDVL         183         9           16         X         7         CQLDPARDVL         184         10           17         POL         622         CQRIVGLL         185         8           17         POL         682         CQRIVGLLGFA         186         11           19         POL         684         CQVFADAT         187         8           20         BNV         310         CTCIPIPSSWA         189         11           20         BNV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9	2	15	<u>}</u>	239	CLRRFIIFLFI	180	Ξ	0.0004				
18         NUC         107         CLTFGRETY         182         9           16         X         7         CQLDPARDVL         183         9           16         X         7         CQLDPARDVL         184         10           17         POL         622         CQRIVGLL         185         8           17         POL         682         CQRIVGLLGFA         186         11           19         POL         684         CQVFADAT         187         8           19         POL         684         CQVFADATPT         188         10           20         BNV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9	0	18	3	107	CLTFGRET	181	œ					
16         X         7         CQLDPARÔV         183         9           16         X         7         CQLDPARDVL         184         10           17         POL         622         CQRIVGLL         185         8           17         POL         682         CQRIVGLLGFA         186         11           19         POL         684         CQVFADAT         187         8           19         POL         684         CQVFADATPT         188         10           20         BNV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9	0	18	3	107	CLTFGRETY	182	6	0.0001				
16         X         7         CQLDPARDVL         184         10           17         POL         622         CQRIVGLL         185         8           17         POL         622         CQRIVGLLGFA         186         11           19         POL         684         CQVFADAT         187         8           19         POL         684         CQVFADATPT         188         10           20         BNV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9	0	16	×	7	COLDPARDV	183	6					
17         POL         622         CQRIVGIL         185         8           17         POL         622         CQRIVGILGFA         186         11           19         POL         684         CQVFADAT         187         8           19         POL         684         CQVFADATPT         188         10           20         BNV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9	0	16	×	7	COLDPARDVL	184	01					
17 POL 622 CQRIVGLIGFA 186 11 19 POL 684 CQVFADAT 187 8 19 POL 684 CQVFADATPT 188 10 20 BNV 310 CTCIPIPSSWA 189 11 19 POL 689 DATPTGWGL 190 9	D.	17	ಕ	622	CORIVGIL	185	80					
19         POL         684         CQVFADAT         187         8           19         POL         684         CQVFADATPT         188         10           20         BAV         310         CTCIPIPSSWA         189         11           19         POL         689         DATPTGWGL         190         9	S	17	절	622	CQRIVGLLGFA	186						
19 POL 684 CQVFADATPT 188 10 20 BNV 310 CTCIPIPSSWA 189 11 19 POL 689 DATPTGWGL 190 9	2	19	젙	684	CQVFADAT	187	80					
20 ENV 310 CTCIPIPSSWA 189 11 19 POL 689 DATPTGWGL 190 9	ς.	19	절	684	CQVFADATPT	188	10					
19 POL 689 DATPTGWGL 190 9	0	20	<u>}</u>	310	CTCIPIPSSWA	189	Ξ					
	വ	19	전	689	DATPTGWGL	190	თ	0.0001				

Table VIII			HBV A02 SU	SUPER MOTIF (With binding information)	With bindin	g informa	tion)			
servancy Frequency	ncy Protein	Position	Sequence	SEQ ID NO:	AA	A.0201	A.0202	A.0203	A.0206	A.6802
9+	8	0	A LOWINGTON	101	,					
75 16	₹ 8	600	DATPTGWGLA	181	<u> </u>					
2 - 2	2 2		DIDPYKEEGA	193						
85 17	3	29	DLLDTASA	194	° ∞					
85 17	NC NC	29	DLLDTASAL	195	o	0.0001				
95 19	ğ	40	DUNIGNILM	196	6	0.0004				
95 19	절	40	DLNLGNLNVSI	197	Ξ					
80 16	NC	32	DTASALYREA	198	10					
	SEC SEC	32	DTASALYREAL	199	-					
95 19	<b>×</b>	14	DVLCLRPV	200	©					
	×	14	DVLCLRPVGA	201	10	0.0001				
	절	541	DVVLGAKSV	202	6	0.0003				
	정	17	EAGPLEEEL	203	6	0.0001				
	×	122	ELGEEIPL	204	æ					
	ğ	718	ELLAACFA	205	œ					
	S N	142	ETVLEYLV	506	œ					
	절	687	FADATPTGWGL	207	==					
	정	724	FARSRSGA	208	80					
	절	821	FASPLHVA	509	89					
	ಕ್ಷ	396	FAVPNLOSL	210	6					
	절	396	FAVPNLQSLT	211	10	0.0003				
	<b>&amp;</b>	243	FIIFLFIL	212	œ	9000.0				
	<b>≥</b>	243	FIIFLFILL	21.3	o	0.0002				
	2	243	FIIFLFILLL	214	10	0.0012				
	<b>≥</b>	248	FILLCLI	215	80	0.0003				
	<b>₩</b>	248	FILLCLIFL	216	10	0.0280				
	<b>№</b>	248	FILLCLIFLL	217	=	0.0010				
	<b>₩</b>	246	FLFILLCL	218	6	0.0002				
80 16	<b>₩</b>	246	FLFILLCLI	219	10	0.0013				
	2	171	FIGPLIN	220	8					
	2	171	FLGPLLVLOA	221	10	0.0190				
	절	513	FLLAQFTSA	222	თ	0.2400				
	절	513	FLLAQFTSAI	223	10	0.2100	0.0320	7.0000	0.1100	0.0880
	정	562	FLLSLGIHL,	224	თ	0.6500	0.0010	0.0100	0.1100	0.0035
	2	183	FLLTRILT	225	œ					
	<b>№</b>	183	FLLTRILTI	226	6	0.5100	0.0430	8.0000	0.2000	0.0010
	<b>8</b>	256	FLIVLLDYOGM	227	=					
	젙	363	FLVDKNPHNT	228	10	0.0012				
95 19	정	656	FTFSPTYKA	229	o,	0.0056	0.0150	0.0031	0.8000	7.3000
	전	. 959	. FTFSPTYKAFL	230	=					
	전	59	FTGLYSST	231	89					
	ದ್ದ	29	FTGLYSSTV	232	თ	0.0005				

National Position   Sequence   National Position   National Positional Positio	Position   SECID   A   A   A   C   C   C   C   C   C   C											
5.2         HLSJFGLPVCA         275         11         6.2200         0.0003         0.9300         0.1700           4.91         HLSPFRILL         276         11         0.2200         0.0003         0.9300         0.1700           7.15         HLRELLAA         278         11         0.0001         0.0001         0.0100         0.0100           5.2         HTALPOAL         281         9         0.0001         0.0001         0.0100         0	5.2         HLSURGLPVCA         275         11	ō		Position	Sequence	SEQ ID NO:	AA	A-0201	A.0202	. A*0203	A.0206	A.6802
491         H.V.SHPII         276         8         0.7200         0.0903         0.1700           715         H.V.SHPIII         277         9         0.2200         0.0903         0.1700           5.2         HTALLAACKA         280         8         0.0001         0.0001         0.0001           5.2         HTALDAACKA         281         9         0.0001         0.0001         0.0001           14.9         HTALLAACKA         282         9         0.0001         0.0001         0.0001           24.1         HTALLA         282         9         0.0002         0.0002         0.1300           24.4         HFELLL         286         11         0.0002         0.0002         0.1300           24.4         HFELLL         286         10         0.0002         0.0002         0.1300           24.4         HELLLL         286         10         0.0002         0.0002         0.1300           24.9         HLCHILL         286         10         0.0002         0.1300         0.1300           24.9         HLCHILL         289         1         0.0002         0.0001         0.1300           24.9         HLCHILL         289	491         H.YSPIPII         276         8         0.2200         0.0003         0.1700           715         H.YSPIPII         277         9         0.2200         0.0003         0.1700           5.2         H.ALELLAAFA         278         11         0.0001         0.0001         0.0001           5.2         H.ALELLAAFA         282         8         0.0001         0.0001         0.0001           5.2         H.ALELLAAFA         283         9         0.0001         0.0001         0.0001           2.4         H.LALLACA         284         9         0.0001         0.0002         0.0004           2.4         H.LALLACA         284         9         0.0001         0.0002         0.0004           2.4         H.LALLACA         284         9         0.0002         0.0002         0.0002           4.9         H.LALLACA <td< td=""><td>×</td><td></td><td>52</td><td>HI SI BGI PVCA</td><td>275</td><td>11</td><td></td><td></td><td></td><td></td><td></td></td<>	×		52	HI SI BGI PVCA	275	11					
491         H-VSHPILL         277         9         0.2200         0.0003         0.8300         0.1700           715         HTAELLAAR         278         11         0.2200         0.0003         0.8300         0.1700           52         HTALROAL         280         8         0.0001         0.0001         0.1700           143         HTUMKGIL         281         9         0.0001         0.0001         0.0001           244         HTUMKGIL         284         8         0.0002         0.0002         0.0004           244         HFILLL         284         8         0.0002         0.0002         0.0004           244         HFILLL         284         11         0.0002         0.0002         0.1300           244         HFILLL         284         10         0.0002         0.0002         0.1300           244         HFILLL         284         10         0.0002         0.0002         0.1300           495         LOWGEN         289         10         0.0002         0.1300         0.1300           498         LOWGEN         289         11         0.0002         0.1300         0.1300           249         L	14   HVSHPHI   17   17   18   18   18   18   18   18	8	پ	491	HLYSHPII	276	; œ		. •			
715         HTAELLAACFA         278         11           52         HTAELLAACFA         279         11           52         HTALLAACFA         281         8           52         HTALLAACFA         281         8         0.0001           54         HTALLAACFA         281         8         0.0001           244         HTWAGIL         282         8         0.0002           244         HTLALL         286         11         0.0002           244         HTCHILLC         286         11         0.0002           244         HTCHILLC         286         11         0.0002           244         HTCHILLC         286         11         0.0002           244         HTCHILL         286         11         0.0002           244         HTCHILL         286         11         0.0002           244         HTCHILL         286         10         0.0002           249         HLCGFRKIM         289         10         0.0002           249         LLCGFRKIM         290         10         0.0005           249         LLCCLIC         292         10         0.0016	715         H/KELLAA         278         8           52         H7ALLAACFA         279         11           52         H7ALROAI         281         9         0.0001           54         H7ALROAI         281         9         0.0001           149         HTUMKGIL         282         8         0.0001           244         HFFILL         285         9         0.0002           244         HFFILL         286         11         0.0002           497         HICFRING         286         10         0.0002           497         HICFRICK         286         10         0.0002           498         LGFRIGHA         289         10         0.0002           497         HICFRICK         289         10         0.0002           498         LGAGNA         289         10         0.0002           499         LLGFIRING         289         10         0.0001           249         LLGFIRICK         289         11         0.0002           249         LLGFIRIT         289         10         0.0001           249         LLGFIRIT         289         11         0.0002 <t< td=""><td>8</td><td>ر</td><td>491</td><td>HLYSHPIIL</td><td>277</td><td>6</td><td>0.2200</td><td>0.0003</td><td>0.9300</td><td>0.1700</td><td>0.0530</td></t<>	8	ر	491	HLYSHPIIL	277	6	0.2200	0.0003	0.9300	0.1700	0.0530
715         HTRELLANCEA         279         111           52         HTALFOAM         280         8         0.0001           52         HTALFOAM         281         8         0.0001           52         HTALFOAM         281         8         0.0001           149         HTIVWAGI         283         9         0.0001           244         HTFLLL         286         9         0.0002           244         HFFLLL         286         9         0.0002           249         HLGFR         288         10         0.0002           249         HLGFR         289         10         0.0015           249         HLCGFR         299         10         0.0016           249         HLCGFR         299         10         0.0016           249         LLCGFR         299         10         0.0016           249         LLCGFR         299         0.0001         0.0002	715         HTARLLAACRA         279         11           52         HTARLLAACRA         280         81           52         HTARLLAACRA         281         8           52         HTARLAAL         281         9           52         HTARCALL         281         9         0.0001           143         HTUMAGAI         282         9         0.0001           244         HFLILL         284         9         0.0002           244         HFLALL         286         9         0.0002           497         ILGFRIA         286         10         0.0002           498         LCMGELM         289         9         0.0002           499         LLCGRILLCL         286         10         0.0015           498         LLCGRILL         289         1         0.0016           499         LLCGRILL         291         9         0.0016           249         LLICCHILL         291         1         0.0016           249         LLICCHILL         291         1         0.0016           249         LLICCHILL         291         1         0.0016           249         LLICCHILL<	8		715	HTAELLAA	278	· &					
5.2         HTALPOAL         280         8           5.2         HTALPOAL         281         9         0.0001           1.49         HTWARGIL         283         9         0.0001           2.44         IIFFILL         284         8         0.0002           2.44         IIFFILL         286         11         0.0002           2.44         IIFFILL         286         11         0.0002           497         ILGFRIGHA         289         8         0.0002           498         LGCFRICHA         289         8         0.0002           249         LLCCHEL         291         9         0.0002           249         LLCCHEL         292         10         0.0005           249         LLCCHEL         292         11         0.0056           249         LLCCHELL         292         10         0.0016           249         LLCCHELL         293         11         0	5.2         HTMPROAL         280         8           1.49         HTWMAGIL         281         9         0.0001           1.49         HTWMAGIL         283         9         0.0001           2.44         IHFFILL         284         8         0.0002           2.44         IHFFILL         286         11         0.0002           2.44         IHFFILL         286         11         0.0002           497         ILGFRIGHM         288         10         0.0002           497         ILGFRIGHM         289         8         0.0002           497         ILGFRIGHM         289         8         0.0002           498         LLGFRIGHM         289         8         0.0002           498         LLGFRIGHM         289         8         0.0001           249         LLGFRIGHM         299         9         0.0001           249         LLGFRIGHM         299         10         0.0001           249         LLCGHMM         299         10         0.0001           249         LLGFRIGHM         299         10         0.0001           249         LLGFRIGHT         299         10	8	ų	715	HTAELLAACFA	279	=					
5.2         HTUMCAGIL         281         9         0.0001           1.49         HTUMCAGIL         282         9         0.0001           2.44         III-THILL         284         8         0.0001           2.44         III-THILL         286         9         0.0002           2.44         III-THILL         286         11         0.0002           2.44         III-THILL         286         10         0.0002           2.44         III-THILL         286         10         0.0002           2.44         III-THILL         286         10         0.0002           2.49         ILLCHILL         287         9         0.0015           2.49         ILLCHILL         287         9         0.0015           2.49         ILLCHILL         287         10         0.016           2.49         ILLCHILL         287         11         0.0015           2.49         ILLCHILL         287         11         0.0016           2.49         ILLCHILL         287         9         0.0016           2.40         ILLCHILL         287         1         0.0016           2.10         ILLCHILL         <	5.2         HTUMORUL         281         9         0.0001           1.49         HTUMKGI         282         8         0.0001           2.44         HTEFLLL         284         8         0.0001           2.44         HFFLLLC         286         11         0.0002           4.97         HIGFRAIL         286         11         0.0002           4.97         HIGFRAIL         286         10         0.0015           4.97         HIGFRAIL         289         10         0.0015           2.49         HLGLEH         291         9         0.0015           2.49         HLCLEL         291         9         0.0016           2.49         HLCLEL         291         9         0.0016           2.49         HLCLEL         291         11         0.0016           2.49         HLCLEL         292         10         0.0166           2.49         HLCLEL         293	z	Q	52	HTALROAI	280	æ					
149   HTUWAGG  282 8 0.0001     244   INFLICIT.   284 8 0.0004     244   INFLICIT.   285 9 0.0002     244   INFLICIT.   286 11 0.0002     245   ILCARIMM 289 8 0.0002     249   ILCARIMM 289 8 0.0001     250   ILCARIMM 289 8 0.0001     251   292   10 0.0056     252   ILCARIMM 289 8 0.0001     253   ICARIMM 289 8     254   ILCARIMM 289 8     255   ICARIMM 289 8 0.0001     251   ICARIMM 289 8 0.0001     252   ICARIMM 289 8 0.0001     253   ICARIMM 289 8 0.0001     254   ICARIMM 289 8 0.0001     255   ICARIMM 289 8 0.0001     256   ICARIMM 289 8 0.0001     257   ICARIMM 289 8 0.0001     258   ICARIMM 289 8 0.0001     259   ICARIMM 289 8 0.0001     250   ICARIMM 289 8 0.0001     251   ICARIMM 289 8 0.0001     252   ICARIMM 289 8 0.0001     253   ICARIMM 289 8 0.0001     254   ICARIMM 289 8 0.0001     255   ICARIMM 289 8 0.0001     256   ICARIMM 289 8 0.0001     257   ICARIMM 289 8 0.0001     258   ICARIMM 289 8 0.0001     259   ICARIMM 289 8 0.0001     250   ICARIMM 289 8 0.0001     251   ICARIMM 289 8 0.0001     252   ICARIMM 289 8 0.0001     253   ICARIMM 289 8 0.0001     254   ICARIMM 289 8 0.0001     255   ICARIMM 289 8 0.0001     256   ICARIMM 289 8 0.0001     257   ICARIMM 289 8 0.0001     258   ICARIMM 289 8 0.0001     259   ICARIM 289 8 0.0001     250   ICARIM 289 8 0.0001     250   ICARIM 289 8 0.0001     251   ICARIM 289 8 0.0001     252   ICARIM 289 8 0.0001     253   ICARIM 289 8 0.0001     254   ICARIM 289 8 0.0001     255   ICARIM 289 8 0.0001     256   ICARIM 289 8 0.0001     257   ICARIM 289 8 0.0001     258   ICARIM 289 8 0.0001     259   ICARIM 289 8 0.0001     250   ICARIM 289 8 0.0001     251   ICARIM 289 8 0.0001     252   ICARIM 289 8 0.0001     253   ICARIM 289 8 0.0001     254   ICARIM 289 8 0.000	149   HTWWAGI   282   8   0.0001     244   IFFILL   284   8   0.0004     244   IFFILL   285   9   0.0002     244   IFFILL   286   11   0.0002     244   IFFILL   286   11   0.0002     245   ILGFRIA   286   11   0.0002     249   ILGFRIA   288   10   0.0001     249   ILCOKELM   289   8   0.0001     249   ILLCUFIL   292   10   0.0015     249   ILLCUFIL   292   10   0.0015     249   ILLCUFIL   293   11   0.0056     249   ILLCUFIL   293   11   0.0056     249   ILLCUFIL   293   11   0.0056     240   ILLCUFIL   293   11   0.0056     251   ILCOKELM   293   11   0.0001     252   ILCOKELM   293   11   0.0001     253   ILCOKELM   294   11   0.0001     254   ILLCUFIL   293   11   0.0001     255   ILLCUFIL   293   11   0.0001     256   ILLCUFIL   293   11   0.0001     257   ILLCUFIL   294   11   0.0001     258   ILLCUFIL   294   0.0001     259   ILLCUFIL   294   0.0001     250   ILLCUFIL   294   0.0001     250   ILLCUFIL   294   0.0001     251   ILLCUFIL   294   0.0001     252   ILLCUFIL   294   0.0001     253   ILLCUFIL   294   0.0001     254   ILLCUFIL   294   0.0001     255   ILLCUFIL   294   0.0001     256   ILLCUFIL   294   0.0001     257   ILLCUFIL   294   0.0001     258   ILLCUFIL   294   0.0001     259   ILLCUFIL   294   0.0001     250   ILLCUFIL   294   0.0001   0.0001     250   ILLCUFIL   294   0.0001   0.0001     250   ILLCUFIL   294   0.0001   0.0001   0.0001     250   ILLCUFIL   294   0.0001   0.0001   0.0001     250   ILLCUFIL   294   0.0001   0.0001   0.0001   0.0001   0.0001   0.0001   0.0001   0.0001   0.0001   0.0001   0.0001   0.0001   0.000	Ź	Q	52	HTALROAIL	281	6	0.0001				
149         HTLWAKGIL         283         9         0.0001           244         IIFFILL         284         8         0.0002           244         IIFFILL         285         9         0.0002           437         IIGFRIAM         286         11         0.0002           497         IIGFRIAM         286         10         0.0002           497         IIGFRIAM         289         8         0.0002           497         IIGFRIAM         289         9         0.0002           497         IIGFRIAM         289         9         0.0002           249         ILLCIII         291         9         0.0015           249         ILLCIII         291         9         0.0016           249         ILLCIII         291         9         0.0016           249         ILLCIIII         293         11         0.0056         0.0001           249         ILLCIIII         294         1         0.0066         0.0001         0.0001           250         ILSTLETTY         296         8         0.0001         0.0001         0.0100           139         ILSTLETTY         296         1	149         HTLWAKGIL         283         9         0.0001           244         IIFLILL         284         8         0.0002           244         IIFLILL         285         11         0.0002           497         IIICFRICH         286         10         0.0002           497         IIICFRICH         286         10         0.0002           497         IIICFRICH         289         8         0.0002           498         IICFRICH         289         9         0.0002           498         IICFRICH         291         9         0.0015           249         IILCCIFIL         291         9         0.0016           249         IILCCIFIL         291         9         0.0016           249         IILCCIFIL         291         11         0.0066           249         IILCCIFIL         293         11         0.0066           249         IILCCIFIL         294         8         0.0001           249         IIICTIFIC         295         11         0.0066         0.0770         0.1300           139         IISTIPETTY         296         11         0.0011         0.0011         0.0	٣	<u>ہ</u>	149	HTLWKAGI	282	80					
244         II-FEILL         284         8         0.0004           244         II-FEILLC         285         9         0.0002           244         II-CHILLCL         286         11         0.0002           244         II-CHENIZH         288         10         0.0002           497         II-CFEKKIPM         288         10         0.0002           498         LICAPRIAN         289         8         0.0002           249         LICAPRIAN         280         9         0.0002           249         LICAPRIAN         289         11         0.0056         0.1300           249         LILLCLFILL         292         10         0.0160         0.0002         0.1300           249         LILLCLFILL         292         11         0.0056         0.0001         0.0002           249         LILLCLFILL         292         10         0.0056         0.0160         0.1300           249         LILLCLFILL         292         10         0.0056         0.0160         0.1300           249         LILLCLFILL         292         10         0.0056         0.0160         0.1300           240         LISTLEFITY	244         III-PILLIL         284         8         0.00004           244         III-PILLIL         286         9         0.0002           244         III-PILLIL         286         11         0.0002           497         IIICFRIEN         289         8         0.0002           497         IIICFRIEN         289         9         0.0002           497         IIICFRIEN         289         9         0.0001           498         ILCMEL         291         9         0.0015           249         ILLICLIFIL         291         9         0.0016           249         ILLICLIFIL         291         9         0.0016           249         ILLICLIFIL         292         10         0.016           249         ILLICLIFIL         293         11         0.0056           249         ILLICLIFIL         293         11         0.0056           250         ILLICLIFIL         294         8         0.0001           260         ILLGIFIL         295         11         0.0056           270         ILLOTIFICH         295         11         0.0051           280         ILLATIFICH         <	ď	ಕ	149	HTLWKAGIL	283	6	0.0001				
244         II-FILLIL         285         9         0.0002           497         III-CERNO         286         11         0.0002           497         III-CERNO         288         10         0.0002           498         III-CERNORM         289         10         0.0002           498         III-CERNORM         289         9         0.0002           498         III-CERNORM         289         10         0.0002           249         III-CERNORM         289         10         0.0015           249         III-CERNORM         289         11         0.0016           249         III-CERNORM         289         11         0.0056         0.1300           249         III-CERNORM         289         11         0.0066         0.1300         0.1300           760         II-STIDETTY         289         10         0.0066         0.0071         0.1300           139         ILSTIDETTY         287         9         0.0001         0.001         0.1300           139         ILSTIDETTY         289         10         0.0001         0.0001         0.001           150         ILSTIDETTY         289         10	244         IIFFILLIL         286         9         0.0002           497         IIGFRIQH         286         11         0.0002           497         IIGFRIQH         289         8         0.0002           498         IIGFRIQH         289         8         0.0002           498         IIGFRIQH         299         9         0.0005           249         ILLCUFL         292         10         0.0190         0.0002           249         ILLCUFL         292         10         0.0160         0.0005           249         ILLCUFL         293         11         0.0005         0.1300           139         ILSTRETY         294         8         0.0001         0.0001           139         ILSTRETY         293         11         0.0001         0.0001           148         ILTPOSL         300         8         0.0001         0.0001 <t< td=""><td>Ш</td><td>≩</td><td>244</td><td>IFLFILL</td><td>284</td><td>80</td><td>0.0004</td><td></td><td></td><td></td><td></td></t<>	Ш	≩	244	IFLFILL	284	80	0.0004				
244         IIFFELLICL         286         11         0.0002           497         ILGFRIGH         287         8         6           497         ILGFRIGH         289         8         10           497         ILGCFRIGH         289         8         0.0002           498         LICCHICL         291         10         0.0162           249         ILLCLIFL         292         10         0.0160         0.1300           249         ILLCLIFL         293         11         0.0056         0.0130         0.0130           249         ILLCLIFL         293         11         0.0056         0.0130         0.1300           249         ILLCLIFL         293         11         0.0056         0.0100         0.1300           760         LRGTSPAYV         295         10         0.0160         0.0001         0.0100           139         LSTLPETT         296         10         0.0210         0.0005         0.1310           139         LSTLPETTY         298         10         0.0011         0.0005         0.0100           139         LSTLPETTY         299         10         0.0016         0.0001         0.0100 <td>244         II-FFILLICL         286         11         0.0002           497         III-CRRICHM         287         8         0.0002           497         III-CRRICHM         288         10         0.0015           497         III-CRRICHM         289         9         0.0005           497         III-CRRICHM         289         9         0.0015           498         III-CLRIL         291         9         0.0015           249         III-CLRIL         291         9         0.0016           249         III-CLRIL         291         9         0.0016           249         III-CLRIL         292         10         0.0160         0.1300           249         III-CLRIL         293         11         0.0056         0.1300         0.1300           250         II-CRRITION         298         10         0.0016         0.0016         0.1300           139         ILSTIPETTY         298         11         0.0021         0.0016         0.1100           139         ILSTIPETTY         298         11         0.0011         0.0011         0.0011           148         ILTIPOSL         300         8</td> <td>ш</td> <td>≱</td> <td>244</td> <td>IIFLFILL</td> <td>285</td> <td>6</td> <td>0.0002</td> <td></td> <td></td> <td></td> <td></td>	244         II-FFILLICL         286         11         0.0002           497         III-CRRICHM         287         8         0.0002           497         III-CRRICHM         288         10         0.0015           497         III-CRRICHM         289         9         0.0005           497         III-CRRICHM         289         9         0.0015           498         III-CLRIL         291         9         0.0015           249         III-CLRIL         291         9         0.0016           249         III-CLRIL         291         9         0.0016           249         III-CLRIL         292         10         0.0160         0.1300           249         III-CLRIL         293         11         0.0056         0.1300         0.1300           250         II-CRRITION         298         10         0.0016         0.0016         0.1300           139         ILSTIPETTY         298         11         0.0021         0.0016         0.1100           139         ILSTIPETTY         298         11         0.0011         0.0011         0.0011           148         ILTIPOSL         300         8	ш	≱	244	IIFLFILL	285	6	0.0002				
497         ILGFRIKI         287         8           497         ILGFRIKIM         288         10           59         LLCMCHEL         289         9         0.0002           498         LLCMCHEL         290         9         0.0001           249         LLLCLIFL         291         9         0.0005           249         LLLCLIFL         292         10         0.0196         0.0130           249         LLLCLIFL         293         11         0.0056         0.0130         0.1300           249         LLLCLIFL         293         11         0.0056         0.0001         0.0002           249         LLLCLIFL         293         11         0.0056         0.0130         0.1300           249         LLLCLIFL         293         10         0.0061         0.0001         0.0002           139         LSTLPETT         294         8         0.0001         0.0001         0.0100           139         LSTLPETT         294         8         0.0001         0.0001         0.0100           148         LTMCST         300         8         0.0001         0.0001         0.0001           153	497         ILGFRIA         287         8           497         ILGFRIAM         288         10           59         LOGODO         10         10           498         LLGFRIAM         290         9         0.0002           249         LLLCUFLL         291         9         0.0015           249         LLLCUFLL         293         11         0.0056         0.1300           139         LLSTLPET         296         8         0.0001         0.0001           139         LSTLPETY         299         11         0.0001         0.0001           139         LSTLPETY         299         11         0.0001         0.0001           139         LSTLPETY         299         0.0001         0.0009         0.0001           148         LSTLPETY         299         11         0.0009         0.0001           153         KAGILYKRET         3	ш	≵	244	IIFLFILLCL	286	=	0.0002				
497         ILCFPKIPM         288         10           498         ILCFPKIPM         289         8           498         LLCLIFL         291         9         0.0005           249         ILCFRGEM         291         9         0.0005           249         ILCLIFL         291         10         0.0160         0.1300           249         ILLCLIFL         292         10         0.0160         0.0001         0.1300           249         ILLCLIFL         293         11         0.0056         0.0001         0.1300           760         ILRGISPAY         294         1         0.0056         0.0001         0.1300           760         ILRGISPAY         295         10         0.0066         0.0001         0.1300           139         LSTLPETT         295         1         0.0001         0.0001         0.1000           139         LSTLPETT         296         1         0.0001         0.0001         0.0001           139         LSTLPETT         296         1         0.0001         0.0001         0.0001           148         LTPOSL         301         0         0.0001         0.0001         0.0001	497         ILGFRAPM         288         10           59         LLCWGELM         289         8           59         LLCWGELM         289         8           498         ILGFRAPM         291         9         0.0005           249         ILLCLIFLL         291         10         0.0150         0.1300           249         ILLCLIFLL         293         11         0.0056         0.0001         0.0002         0.1300           249         ILLCLIFLL         294         11         0.0056         0.0001         0.0002         0.1300           249         ILLCLIFLL         294         1         0.0056         0.0001         0.0002         0.1300           139         ILSTLPETT         294         10         0.0016         0.0001         0.0002         0.1300           139         ILSTLPETT         294         10         0.0210         0.0005         0.0100           139         ILSTLPETTY         294         10         0.0011         0.0065         0.0770         0.3100           139         ILSTLPETTY         294         10         0.0001         0.0001         0.0001           156         ILYKRETT	_	ಶ	497	ILGFRKI	287	΄ α					
59         LCWGELM         289         8           498         LCWGELM         289         8           498         LICCHELL         290         9         0.0002           498         LICCHELL         291         9         0.0001           249         LILLCHELL         292         10         0.0016         0.0180         0.1300           249         LILLCHELL         293         11         0.0056         0.0001         0.0002         0.1300           249         LILLCHELL         293         11         0.0056         0.0001         0.0002         0.1300           249         LILLCHELL         293         10         0.0056         0.0001         0.0002         0.1300           39         LISTLEETT         296         10         0.0011         0.0001         0.0100           139         LISTLEETT         296         10         0.0001         0.0001         0.0100           139         LISTLEETT         299         10         0.0001         0.0001         0.0100           139         LISTLEETT         299         10         0.0001         0.0001         0.0100           150         MGLGFAA         <	59         LLOWGELM         289         8           498         LEGRENIAM         290         9         0.0002           498         LEGRENIAM         290         9         0.0002           249         ILLCLIFIL         292         10         0.0190         0.0001         0.1300           249         ILLCLIFIL         293         11         0.0056         0.0190         0.0130         0.1300           249         ILLCLIFILL         293         10         0.0160         0.0005         0.1300           760         ILRGISPAY         294         8         10         0.0160         0.0160           760         ILRGISPAY         295         10         0.0160         0.0160         0.1300           139         ILSTIPETT         297         9         0.0001         0.0210         0.0770         0.3100           139         ILSTIPETTY         298         10         0.0001         0.0001         0.001           139         ILSTIPETTY         299         10         0.0001         0.0001         0.0001           150         INCLICKAN         302         9         0.0001         0.0001         0.0001		절	497	IILGFRKIPM	288	10					
498         ILGFRKIPM         290         9         0.0002           249         ILLICUFIL         291         9         0.0015           249         ILLICUFIL         292         10         0.0019         0.0001           249         ILLICUFILL         293         11         0.0066         0.1300         0.1300           249         ILLICUFILL         294         8         0.0016         0.0066         0.1300         0.1300           139         ILSTILPETT         296         10         0.0010         0.0085         0.0770         0.3100           139         ILSTILPETTY         296         10         0.0210         0.0085         0.0770         0.3100           139         ILSTILPETTY         299         11         0.0210         0.0085         0.0770         0.3100           188         ILSTILPETTY         299         11         0.0210         0.0091         0.0010 </td <td>498         ILGFRKIPM         290         9         0.0002           249         ILLICUEL         291         9         0.0005           249         ILLICUELL         292         10         0.0015         0.0130           249         ILLICUELL         292         10         0.0056         0.1300           249         ILLICUELL         293         11         0.0056         0.1300           760         ILRGTSFVV         294         8         0.0066         0.0077         0.1300           139         ILSTILETT         297         9         0.0001         0.0077         0.3100           139         ILSTILETTY         298         10         0.0001         0.0210         0.0770         0.3100           139         ILSTILETTY         298         11         0.0210         0.0085         0.0770         0.3100           189         ILTIPOSL         300         8         0.0001         0.0001         0.0001           153         KAGILYKHETT         304         10         0.0001         0.0001         0.0001         0.0001           153         KAGILYKHETT         306         9         0.0001         0.0001         0.00</td> <td></td> <td>3</td> <td>59</td> <td>ILCWGELM</td> <td>289</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	498         ILGFRKIPM         290         9         0.0002           249         ILLICUEL         291         9         0.0005           249         ILLICUELL         292         10         0.0015         0.0130           249         ILLICUELL         292         10         0.0056         0.1300           249         ILLICUELL         293         11         0.0056         0.1300           760         ILRGTSFVV         294         8         0.0066         0.0077         0.1300           139         ILSTILETT         297         9         0.0001         0.0077         0.3100           139         ILSTILETTY         298         10         0.0001         0.0210         0.0770         0.3100           139         ILSTILETTY         298         11         0.0210         0.0085         0.0770         0.3100           189         ILTIPOSL         300         8         0.0001         0.0001         0.0001           153         KAGILYKHETT         304         10         0.0001         0.0001         0.0001         0.0001           153         KAGILYKHETT         306         9         0.0001         0.0001         0.00		3	59	ILCWGELM	289						
249         ILLICUFIL         291         9         0.0015           249         ILLICUFIL         292         10         0.0190         0.0002         0.1300           249         ILLICUFILL         293         11         0.0056         0.0001         0.0130         0.1300           760         ILRGTSFWY         294         8         10         0.0160         0.1300         0.1300           760         ILRGTSFWY         295         10         0.0016         0.0160         0.13100           139         ILSTLPETT         297         9         0.0001         0.0210         0.0770         0.3100           139         ILSTLPETTY         298         10         0.0210         0.0210         0.0770         0.3100           139         ILSTLPETTY         298         10         0.0210         0.0010         0.0310           148         ILTIPOSIL         301         8         0.0001         0.0001         0.0010           625         IVGLIGFAA         302         9         0.0001         0.0001         0.0010           153         KAGILYKRETT         305         11         0.0001         0.0001         0.0010 <t< td=""><td>249         ILLCUFL         291         9         0.0015           249         ILLCUFLL         292         10         0.0166         0.0001         0.0002         0.1300           249         ILLCUFLL         293         11         0.0056         0.0001         0.0130         0.1300           760         ILRGTSFV         294         8         10         0.0160         0.0160         0.1300           760         ILRGTRETY         295         10         0.0160         0.0001         0.0160         0.1310           139         ILSTILPETTY         296         8         0.0001         0.0210         0.0001         0.0100           139         ILSTILPETTY         299         11         0.0001         0.0001         0.0100           139         ILSTILPETTY         299         11         0.0001         0.0001         0.0100           150         ILSTILPETTY         299         11         0.0009         0.0001         0.0100           150         ILSTILPETTY         299         11         0.0009         0.0001         0.0001           150         ILSTILPETTY         303         9         0.00001         0.0001         0.0001</td><td></td><td>텇</td><td>498</td><td>ILGFRKIPM</td><td>290</td><td>თ</td><td>0.0002</td><td></td><td></td><td></td><td></td></t<>	249         ILLCUFL         291         9         0.0015           249         ILLCUFLL         292         10         0.0166         0.0001         0.0002         0.1300           249         ILLCUFLL         293         11         0.0056         0.0001         0.0130         0.1300           760         ILRGTSFV         294         8         10         0.0160         0.0160         0.1300           760         ILRGTRETY         295         10         0.0160         0.0001         0.0160         0.1310           139         ILSTILPETTY         296         8         0.0001         0.0210         0.0001         0.0100           139         ILSTILPETTY         299         11         0.0001         0.0001         0.0100           139         ILSTILPETTY         299         11         0.0001         0.0001         0.0100           150         ILSTILPETTY         299         11         0.0009         0.0001         0.0100           150         ILSTILPETTY         299         11         0.0009         0.0001         0.0001           150         ILSTILPETTY         303         9         0.00001         0.0001         0.0001		텇	498	ILGFRKIPM	290	თ	0.0002				
249         ILLICLIFIL         292         10         0.0190         0.0000         0.1300           249         ILLICLIFILY         293         11         0.0056         0.1300         0.1300           760         ILRGTSPAY         295         10         0.0160         0.0160         0.13100           139         ILSTLPETT         296         10         0.0011         0.0016         0.0170         0.13100           139         ILSTLPETTY         299         10         0.00210         0.0077         0.3100           139         ILSTLPETTY         299         10         0.00210         0.0077         0.3100           139         ILSTLPETTY         299         10         0.0021         0.0077         0.3100           148         ILSTLPETTY         299         10         0.0009         0.0077         0.3100           156         ILSTLPETTY         299         10         0.0009         0.0077         0.3100           158         ILSTLPETTY         304         10         0.0009         0.0071         0.0001           153         KAGILYRETT         305         11         0.00690         0.0074         0.0069           21 </td <td>249         ILLICLIFIL         292         10         0.0190         0.0000         0.1300           249         ILLICLIFILA         293         11         0.0056         0.0001         0.0100         0.1300           760         ILRGITSFAVY         295         10         0.0160         0.0160         0.1300           139         ILSTLPETT         296         10         0.0001         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0210         0.0071         0.0310           139         ILSTLPETTY         299         11         0.0009         0.0071         0.0071           148         ILTROSL         300         9         0.0009         0.0071         0.0071           153         KAGILYKHETT         306         9         0.0009         0.0069         0.0074         0.55900           21         KAGILYKHETT         309         1</td> <td></td> <td>2</td> <td>249</td> <td>ILLICLIFL</td> <td>291</td> <td>6</td> <td>0.0015</td> <td></td> <td></td> <td></td> <td></td>	249         ILLICLIFIL         292         10         0.0190         0.0000         0.1300           249         ILLICLIFILA         293         11         0.0056         0.0001         0.0100         0.1300           760         ILRGITSFAVY         295         10         0.0160         0.0160         0.1300           139         ILSTLPETT         296         10         0.0001         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0210         0.0071         0.0310           139         ILSTLPETTY         299         11         0.0009         0.0071         0.0071           148         ILTROSL         300         9         0.0009         0.0071         0.0071           153         KAGILYKHETT         306         9         0.0009         0.0069         0.0074         0.55900           21         KAGILYKHETT         309         1		2	249	ILLICLIFL	291	6	0.0015				
249         ILLCLIFLLV         293         11         0.0056           760         ILRGTSFV         294         8         6           760         ILRGTSFV         294         8         0.0160           139         ILSTLPETT         296         10         0.0001           139         ILSTLPETTV         298         10         0.0001           139         ILSTLPETTV         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0010         0.0010         0.0010           156         ILYREFT         301         8         0.0009         0.0009         0.0009           153         KAGLIVKRETT         305         11         0.0009         0.0009         0.0009           153         KAGLIVKRETT         305         10         0.0009         0.0009         0.0009           154         KAGLIVKRETT<	249         ILLCLIFLLV         293         11         0.0056           760         ILRGTSFV         294         8         0.0160           760         ILRGTSFV         294         10         0.0160           760         ILRGTSFV         294         10         0.0160           139         ILSTLPETT         296         8         0.0001           139         ILSTLPETT         298         10         0.0210         0.0770         0.3100           139         ILSTLPETTV         298         11         0.0210         0.0071         0.3100           139         ILSTLPETTV         298         11         0.0210         0.0770         0.3100           139         ILSTLPETTV         298         11         0.0210         0.0071         0.0770         0.3100           139         LSTLPETTV         299         11         0.0009         0.0009         0.0009           625         NGLIGARA         302         8         0.0009         0.0009         0.0009           503         KAGILYKRETT         305         11         0.0009         0.0009         0.0009           489         KLHLYSHPIL         310         9		<b>}</b>	249	ILLICLIFIL	292	10	0.0190	0.0001	0.0002	0.1300	0.0015
760         ILRGTSFV         294         8           760         ILRGTSFVY         295         10         0.0160           139         ILSTLPETT         296         10         0.0001           139         ILSTLPETTV         298         10         0.0001           139         ILSTLPETTV         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0001         0.0001         0.0010           150         NGLIGFAA         302         8         0.0009         0.0009         0.0001           625         NGLIGFAA         303         9         0.0009         0.0001           153         KAGILYKRET         306         11         0.0001         0.0001           503         KILHYSHPIL         307         10         0.0090         0.0590         0.5900           489         KILHYSHPIL         310         11         0.0001         0.0001         0.0001           489         KILHYSHPIL         31         9	760         ILRGTSFV         294         8           760         ILRGTSFVY         295         10         0.0160           760         ILRGTSFVY         295         10         0.0160           139         ILSTLPETT         297         9         0.0001           139         ILSTLPETTY         298         10         0.0210         0.0355         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0009         0.0009         0.0009           148         ILTHOSL         302         8         0.0009         0.0009         0.0009           153         KAGILYKRET         304         10         0.0009         0.0001         0.0001           153         KAGILYKRET         306         9         0.0099         0.0099         0.0099         0.0099         0.0099           153         KAGILYKRET         306         9         0.0099         0.0099         0.0		<b>₩</b>	249	ILLICLIFLLY	293	=	0.0056				
760         ILRGTSFYVV         295         10         0.0160           139         ILSTLPET         296         8         0.0001           139         ILSTLPETTY         298         10         0.0010         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTY         299         11         0.0010         0.0070         0.3100           188         ILTPGSL         300         8         0.0009         0.0009         0.0009         0.0009           625         IVGLGFAA         304         10         0.0009	760         ILRGTSFWYV         295         10         0.0160           139         ILSTLPET         296         8         0.0001           139         ILSTLPETT         297         9         0.0001           139         ILSTLPETTV         298         10         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0210         0.0085         0.0770         0.3100           18         ILTPOSL         300         8         0.0009		점	160	ILRGTSFV	294	80					
139   ILSTLPET   296   8   1.5TLPET   297   9   0.0001     139   ILSTLPETTV   298   10   0.0001     139   ILSTLPETTV   298   10   0.0010     139   ILSTLPETTVV   298   10   0.0010     139   ILSTLPETTVV   298   11   0.0011     148   ILTIPOSL   300   8   8   0.0001     150   IVKRETT   301   8   0.0009     151   IVKRETT   302   8   0.0009     152   IVGLIGFA   303   9   0.0009     153   KAGLIVKRETT   305   10   0.0001     153   KAGLIVKRETT   305   8   0.0001     154   KLHLYSHPI   308   9   0.0001     155   KLHVSHPI   310   11   11     156   KLPWINFI   311   8   0.0001     157   KTRIWGYSL   311   8   0.0001     158   KVGORIVGL   314   9   0.0001     159   KVGORIVGL   315   9   0.0001     150   KVGORIVGL   315   9	139         ILSTLPET         296         8           139         ILSTLPETT         297         9         0.0001           139         ILSTLPETTV         298         10         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0009		점	260	ILRGTSFVYV	295	10	0.0160				
139 ILSTIPETT 297 9 0.0001 139 ILSTIPETTV 298 10 0.0210 0.0210 0.03100 139 ILSTIPETTVV 298 11 0.0210 0.0210 0.03100 139 ILSTIPETTVV 299 111 139 ILSTIPETTVV 299 111 150 ILTIPOST 300 8 8 151 ILTIPOST 301 8 9 0.0009 152 IVKRETT 301 8 8 0.00001 153 KAGILVKRETT 305 8 0.00001 153 KAGILVKRETT 305 11 10 153 KAGILVKRETT 306 8 9 0.0690 0.0340 2.7000 0.5900 154 KAGILVKRETT 306 9 0.0690 0.0340 2.7000 0.5900 155 KAGILVKRETT 309 10 0.0001 156 KLHLYSHPIL 310 9 0.0001 157 KTKHWGYGL 311 8 0.0001 158 KCHLYSHPIL 311 8 0.0001 159 KCHLYSHPIL 311 9 0.0001 150 KCAGNWGLL 311 9 0.0001 150 KVCAGNWGLL 311 9 0.0001 150 KVCAGNWGLL 311 8 0.0001 150 KVCAGNWGLL 311 8 0.0001 150 KVCARNGL 315 10 0.0001	139   ILSTLPETT   297   9   0.0001     139   ILSTLPETTV   298   10   0.0210   0.0085   0.0770   0.3100     139   ILSTLPETTVV   299   11   0.0210   0.0085   0.0770   0.3100     188   ILTROSL   300   8   8   8   8   8   8   8   8   8		3	139	LSTLPET	296	80					
139         ILSTLPETTV         298         10         0.0210         0.0085         0.0770         0.3100           139         ILSTLPETTV         299         11         0.0210         0.0085         0.0770         0.3100           188         ILTROSL         300         8         8         0.0009	139         ILSTIPETTV         298         10         0.0210         0.0085         0.0770         0.3100           139         ILSTIPETTV         299         11         0.0210         0.0085         0.0770         0.3100           188         ILTPOSL         300         8         8         0.0009         0.0009         0.0009         0.0009         0.0009         0.0009         0.0009         0.0009         0.0009         0.0001		3	139	ILSTLPETT	297	6	0.0001				
139         ILSTLPETTVV         299         11           188         ILTROSL         300         8           156         ILVKRETT         301         8           625         IVGLIGFAA         302         8           625         IVGLIGFAA         303         9         0.0009           153         KAGILYKRETT         304         10         0.0001           153         KAGILYKRETT         306         8         0.0001           21         KLGGWLWGM         307         10         0.0001           489         KLHLYSHPI         309         10         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         309         10         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         319         9         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         6.0001         1.0         0.0001         1.0         0.0001         1.0         0.0001         1.0         0.0001         1.0         0.0001         1.0         0.0001         0.0001         0.0001         0.	139         ILSTLPETTVV         299         11           188         ILTIPOSL         300         8           156         ILYRRETT         301         8           625         IVGLIGFAA         302         8           625         IVGLIGFAA         303         9         0.0009           625         IVGLIGFAA         303         9         0.0009           625         IVGLIGFAA         303         10         0.0001           625         IVGLIGFAA         303         11         0.0001           603         KAGILYKRETT         306         8         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPI         308         10         0.0690         0.0690         0.0590         0.0590           489         KLHYSHPII         310         11         8         0.0690         0.0690         0.0690         0.0690           489         KLHYSHPII         310         11         8         0.0690         0.0001         0.0690         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001		3	139	LSTLPETTV	298	10	0.0210	0.0085	0.0770	0.3100	0.0067
188         ILTIPOSL         300         8           156         ILYKRETT         301         8           625         NGLIGFAA         302         8           625         NGLIGFAA         303         9         0.0009           153         KAGILYKRETT         304         10         0.0001           153         KAGILYKRETT         305         11         0.0001           153         KIPILYSHPIT         306         8         0.0690         0.0340         2.7000         0.5900           2 1         KLCIGWLWGM         307         10         0.0690         0.0340         2.7000         0.5900           4 89         KLHLYSHPIL         310         11         8         0.0690         0.0340         2.7000         0.5900           4 89         KLHLYSHPIL         310         11         8         0.00690         0.00690         0.00690         0.00690         0.0000         0.5900           4 89         KLHLYSHPIL         310         11         8         0.00690         0.00690         0.00690         0.00690         0.00690         0.00690         0.00690         0.00690         0.00690         0.00690         0.00690         0.00690 <td>188         ILTIPOSL         300         8           156         ILYKRETT         301         8           625         IVGLIGFAA         302         8           625         VGLIGFAA         303         9         0.0009           153         KAGILYKRET         304         10         0.0001           153         KAGILYKRET         305         11         0.0001           153         KAGILYKRET         306         8         0.0001           21         KLCIGWLWGM         307         10         0.0001           489         KLHLYSHPI         309         10         0.0690         0.05340         2.7000         0.5900           489         KLHLYSHPI         309         10         0.0690         0.00340         2.7000         0.5900           489         KLHLYSHPIL         310         11         8         0.0690         0.0091           489         KLHLYSHPIL         310         11         8         0.0001           489         KLHLYSHPIL         310         11         8         0.0001           653         KOAFINICKIL         314         9         0.0001         0.0001           &lt;</td> <td></td> <td>3</td> <td>139</td> <td>ILSTLPETTVV</td> <td>299</td> <td>Ξ</td> <td></td> <td></td> <td></td> <td></td> <td></td>	188         ILTIPOSL         300         8           156         ILYKRETT         301         8           625         IVGLIGFAA         302         8           625         VGLIGFAA         303         9         0.0009           153         KAGILYKRET         304         10         0.0001           153         KAGILYKRET         305         11         0.0001           153         KAGILYKRET         306         8         0.0001           21         KLCIGWLWGM         307         10         0.0001           489         KLHLYSHPI         309         10         0.0690         0.05340         2.7000         0.5900           489         KLHLYSHPI         309         10         0.0690         0.00340         2.7000         0.5900           489         KLHLYSHPIL         310         11         8         0.0690         0.0091           489         KLHLYSHPIL         310         11         8         0.0001           489         KLHLYSHPIL         310         11         8         0.0001           653         KOAFINICKIL         314         9         0.0001         0.0001           <		3	139	ILSTLPETTVV	299	Ξ					
156         ILYKRETT         301         8           625         IVGLIGFA         302         8           625         IVGLIGFAA         303         9         0.0009           153         KACILYKRET         304         10         0.0001           153         KACILYKRETT         305         11         0.0001           21         KACILYKRETT         306         8         0.0001           21         KACILYKRETT         306         8         0.0001           489         KLHLYSHPI         308         9         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPIL         310         11         11         11         8         6.0001         0.0690         0.059	156         ILYKRETT         301         8           625         IVGLIGFAA         302         8           625         IVGLIGFAA         303         9         0.0009           153         KAGILYKRET         304         10         0.0001           153         KAGILYKRET         305         11         0.0001           203         KIPMGYGL         306         8         0.0061           21         KLCLGWLWGM         307         10         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.00690         0.0001         8           489         KLHLYSHPII         312         9         0.0001         0.0001         0.0001           489         KLHLYSHPII         313         9         0.0001         0.0001         0.0001           620         KVCORIVGL         316         8         0.0001         0.0001         0.0001           55         KVGNITGL         316         8         0.0001         0.0001 <td></td> <td>2</td> <td>188</td> <td>ILTIPOSL</td> <td>300</td> <td>80</td> <td></td> <td></td> <td></td> <td></td> <td></td>		2	188	ILTIPOSL	300	80					
625         WGLLGFAA         302         8           625         WGLLGFAA         303         9         0.0009           153         KAGILYKRET         304         10         0.0009           153         KAGILYKRETT         305         11         0.0001           21         KAGILYKRETT         306         8         0.0001           21         KACIGWLWGM         307         10         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPIIL         310         11         8         0.0690         0.00340         2.7000         0.5900           489         KLHLYSHPIIIL         310         11         8         0.0001         8           610         KLPYNHPI         311         8         0.0001         0.0001         0.0001           620         KVCQRINGL         314         9         0.0003         0.0001         0.0001           620         KVCQRINGL         315         9         0.0003         0.0001         0.0001           55         KVGRI	625         IVGLLGFA         302         8           625         IVGLLGFAA         303         9         0.0009           153         KAGILYKRETT         304         10         0.0001           153         KAGILYKRETT         305         11         0.0001           503         KIPMGVGL         306         8         0.0001           2 1         KLCLGWAWGM         307         10         0.0690         0.0590           489         KLHLYSHPIL         310         11         11           489         KLHLYSHPIL         310         11           610         KLDVNRPIL         312         9         0.0001           653         KOAFIFSPT         312         9         0.0003           650         KVCORIVGL         314         9         0.0003           620         KVCORIVGL         315         9         0.0003           620         KVGNFTGL         316         8         0.0001           620         KVGNFTGL         316         8         0.0001		절	156	ILYKRETT	301	ဆ					
625         IVGLLGFAA         303         9         0.0009           153         KAGILYKRET         304         10         0.0009           153         KAGILYKRETT         305         11           503         KIPMGVGL         306         8           21         KLCIGWLWGM         307         10         0.0001           489         KLHLYSHPII         309         10         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0001         0.0001         0.0001           653         KOAFITSPT         312         9         0.0001         0.0001         0.0001         0.0001         0.0001           620         KVCQRIVGL         315         9         0.0001         0.0001         0.0001         0.0001           55         KVGNFTGL         316         8         0.0001         0.0001	625         WGLLGFAA         303         9         0.0009           153         KAGILYKRET         304         10         0.0009           153         KAGILYKRETT         305         11         0.0001           21         KACILYKRETT         306         8         0.0001           21         KLGWLWGM         307         10         0.0690         0.0590           489         KLHLYSHPII         310         11         8           489         KLHLYSHPIIL         310         11         8           610         KLPVNRPI         311         8         0.0001           653         KOAFTFSPT         312         9         0.0001           653         KVCGRIVGL         314         9         0.0003           620         KVCGRIVGL         315         10         0.0001           55         KVGNFTGL         316         8         0.0001		전	625	IVGLLGFA	302	80					
153         KAGILYKRET         304         10           153         KAGILYKRETT         305         11           503         KIPMGVGL         306         8           21         KLCIGWLWGM         307         10         0.0001           489         KLHLYSHPII         309         10         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0001         0.0001           574         KTRRWGYSL         312         9         0.0001         0.0001         0.0001           620         KVCQRIVGL         314         9         0.0001         0.0001         0.0001           55         KVGNFTGL         316         8         0.0001         0.0001         0.0001	153         KAGILYKRET         304         10           153         KAGILYKRETT         305         11           503         KIPMGVGL         306         8           21         KLCIGWLWGM         307         10         0.0001           489         KLHLYSHPII         309         10         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         0.0001         0.0001         0.0001         0.0001           574         KTRRWGYSL         314         9         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001         0.0001		점	625	IVGLLGFAA	303	6	0.0009				
153         KAGILYKRETT         305         11           503         KIPMGVGL         306         8           21         KLCLGWLWGM         307         10         0.0001           489         KLHLYSHPII         309         10         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         6.10         KLPVNRPI         311         8         8         6.53         KOAFTESPT         312         9         0.0001         0.0001         0.0001         6.00001         0.0001	153         KAGILYKRETT         305         11           503         KIPMGVGL         306         8           21         KLCLGWLWGM         307         10         0.0001           489         KLHLYSHPI         309         10         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         6.10         KLPVNRPI         310         11         8         6.53         KOAFTESPT         312         9         0.0001         0.0001         0.0001         6.00001         0.0001		점	153	KAGILYKRET	304	-0					
503         KIPMGVGL         306         8           21         KLCLGWLWGM         307         10         0.0001           489         KLHLYSHPII         308         9         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         11         8         653         KOAFTESPT         312         9         0.0001         0	503         KIPMGVGL         306         8           21         KLCLGWLWGM         307         10         0.0001           489         KLHLYSHPI         308         9         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         11         8         6.10         KLHZHYBPII         8         8         0.0001         0.0001         0.5900         0.		ಕ	153	KAGILYKRETT	305	Ξ					
21         KLCLGWLWGM         307         10         0.0001           489         KLHLYSHPI         308         9         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         11         8         11         8         11         8         12         9         0.0001<	21         KLCLGWLWGM         307         10         0.0001           489         KLHLYSHPI         308         9         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         11         8         6.10         KLPVNRPI         311         8         0.0001		정	503	KIPMGVGL	306	œ					
489         KLHLYSHPI         308         9         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPII         310         11         8         13         8         13         8         13         8         13         14         8         13         14	489         KLHLYSHPI         308         9         0.0690         0.0340         2.7000         0.5900           489         KLHLYSHPIIL         310         11         11         8         11         8         11         8         11         8         12         9         0.0001 <t< td=""><td></td><td>3</td><td>21</td><td>KLCLGWLWGM</td><td>307</td><td>10.</td><td>0.0001</td><td></td><td></td><td></td><td></td></t<>		3	21	KLCLGWLWGM	307	10.	0.0001				
489         KLHLYSHPİL         309         10           489         KLHLYSHPİL         310         11           610         KLPVNRPİ         311         8           653         KOAFTESPT         312         9           574         KTKRWĞYSL         313         9         0.0001           620         KVCQRIVĞL         315         10         0.0001           55         KVĞNFTĞL         316         8	489         KLHLYSHPİİ         309         10           489         KLHLYSHPİİL         310         11           610         KLPVNRPİ         311         8           653         KOAFTESPT         312         9         0.0001           574         KTKRWĞYSL         313         9         0.0001           620         KVCQRIVĞL         315         10         0.0001           55         KVĞNFTĞL         316         8         0.0001		전	489	KLHLYSHPI	308	6	0.0690	0.0340	2.7000	0.5900	0.0015
489         KLHLYSHPIIL         310         11           610         KLPVNRPI         311         8           653         KOAFTFSPT         312         9           574         KTKRWGYSL         313         9           620         KVCQRIVGL         314         9           620         KVCQRIVGLL         315         10           55         KVGNFTGL         8	489         KLHLYSHPIIL         310         11           610         KLPVNRPI         311         8           653         KOAFTFSPT         312         9           574         KTKRWGYSL         313         9           620         KVCARIVGL         314         9           620         KVCARIVGLL         315         10           55         KVGNFTGL         316         8		전	489	KLHLYSHPII	309	9					
610       KLPVNRPI       311       8         653       KQAFTFSPT       312       9         574       KTKRWGYSL       313       9         620       KVCQRIVGL       314       9         620       KVCQRIVGLL       315       10         55       KVGNFTGL       316       8	610       KLPVNRPI       311       8         653       KQAFTFSPT       312       9         574       KTKRWGYSL       313       9         620       KVCQRIVGL       314       9         620       KVCQRIVGLL       315       10         55       KVGNFTGL       316       8		젙	489	KLHLYSHPIIL	310	=					
653       KQAFTFSPT       312       9         574       KTKRWGYSL       313       9         620       KVCQRIVGL       314       9         620       KVCQRIVGLL       315       10         55       KVGNFTGL       316       8	653       KQAFTFSPT       312       9         574       KTKRWGYSL       313       9         620       KVCARIVGL       314       9         620       KVCARIVGLL       315       10         55       KVGNFTGL       316       8		점	610	KLPVNRPI	311	80					
574       KTKRWGYSL       313       9         620       KVCQRIVGL       314       9         620       KVCQRIVGLL       315       10         55       KVGNFTGL       316       8	574       KTKRWGYSL       313       9         620       KVCARIVGL       314       9         620       KVCARIVGLL       315       10         55       KVGNFTGL       316       8		점	653	KOAFTFSPT	312	6					
620 KVCQRIVGL 314 9 620 KVCQRIVGLL 315 10 55 KVGNFTGL 316 8	620 KVCQRIVGL 314 9 620 KVCQRIVGLL 315 10 55 KVGNFTGL 316 8		전	574	KTKRWGYSL	313	o	0.0001				
620 KVCQRIVGLL 315 10 55 KVGNFTGL 316 8	620 KVGARVGLL 315 10 55 KVGNFTGL 316 8		점	. 029	KVCQRIVGL	314	6	0.0003				
55 KVGNFTGL 316 8	55 KVGNFTGL 316 8		절	620	KVCQRIVGLL	315	<del>-</del>	0.0001				
			ಶ	22	KVGNFTGL	316	80					

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Constructive Finquents   Finquents   Finquents   Saguents   No.											
X         91         KNLHGRTL         317         B           AX         94         KNLHGRTL         319         100002           POL         534         LAFSWINDOW         320         10         0.0002           POL         514         LAGFTSANDOW         322         11         0.0003           POL         515         LAGFTSANDOW         322         11         0.0002           POL         515         LAGFTSANDOW         323         11         0.0003           POL         515         LAGFTSANDOW         323         11         0.0003           POL         515         LAGFTSANDOW         323         11         0.0003           POL         516         LAGFTSANDOW         323         11         0.0003           POL         514         LAGFTSANDOW         322         9         0.0003           POL         514         LAGFTSANDOW         323         10         0.0013           POL         514         LAGFTSANDOW         323         10         0.0013           POL         514         10         0.0013         0.0013           POL         514         10         0.0013         0.0014		Protein	Position	Sequence	SEQ ID NO:	AA	A*0201	A*0202	. A*0203	A*0206	A.6802
X         3   VMMPRTICAL         318         10         0.0004           POL         534         LMSSNDDVL         221         11         0.0002           POL         534         LMSSNDDVL         221         11         0.0002           POL         515         LMGPTSAL         322         11         0.0002           POL         514         LMGPTSAL         323         11         0.0002           POL         514         LMGPTSAL         323         11         0.0002           POL         514         LMGPTSAL         325         8         0.1000         0.2700         3.7000         0.2800           POL         514         LMGPTSAL         325         8         0.1000         0.0004         3.7000         0.2800           BW         251         LLCLIFLIA         328         9         0.1004         0.0004           BW         251         LLCLIFLIA         328         9         0.0004         0.0004           BW         251         LLCLIFLIA         329         11         0.0014         0.0004           BW         251         LLCLIFLIA         323         1         0.0004         0.0004 <td>17</td> <td>×</td> <td>91</td> <td>KVLHKRTL</td> <td>317</td> <td>ω</td> <td></td> <td></td> <td></td> <td></td> <td></td>	17	×	91	KVLHKRTL	317	ω					
PCL         534         LAFSWIDDV         319         9         0.0002           PCL         534         LAFSWIDDV         320         10         0.0003           PCL         515         LAFTSWIDDV         321         11         0.0025           PCL         515         LAGTSWIDDV         322         8         0.0026           PCL         514         LAGTSWIDDV         326         9         0.0004         0.2700         3.7000           PCL         514         LAGTSWIDDV         326         9         0.0004         0.2700         3.7000         0.2600           PW         251         LCLAIRLIAL         329         10         0.0004         0.0004         0.0004           PW         251         LCLAIRLIAL         329         10         0.0014         0.0004         0.0004           PW         251         LCLAIRLIAL         329         10         0.0004	17	×	91	KVLHKRTLGL	318	01	0.0004				
PCL         514         LAFSWIDDW         320         110         0.0003           PCL         515         LAGFTSAI         322         11         0.00025           PCL         515         LAGFTSAI         322         11         0.00025           PCL         515         LAGFTSAICS         323         11         0.00025           PCL         514         LLAGFTSAICS         323         11         0.00025           PCL         514         LLAGFTSAICS         325         8         0.1000         0.2700         0.2600           PW         251         LLCLIFL         327         8         0.10004         0.2700         0.2600           BW         251         LLCLIFL         329         10         0.0013         0.0014           BW         251         LLCLIFL         320         10         0.0013         0.0014           BW         251         LLCLIFL         330         11         0.0014         0.0010           PW         250         LLCLIFL         332         11         0.0014         0.0014           PW         250         LLCLIFL         332         8         0.0004         0.0014	18	젙	534	LAFSYMDDV	319	6	0.0002				
PCL         515         LAFSWIDDOWL         321         11           PCL         515         LAGFTSALCSV         322         11           PCL         515         LAGFTSALCSV         322         11           PCL         514         LLAGFTSAL         322         11           PCL         514         LLAGFTSAL         326         9         0.0004           PW         251         LLAGFTSAL         326         9         0.0004           BW         251         LLCAFILL         326         9         0.0004         0.2700         0.2600           BW         251         LLCAFILL         329         10         0.0007         9         0.0007           BW         251         LLCAFILL         329         10         0.0017         0.0007         0.0007           BW         251         LLCAFILL         33         10         0.0017         0.0000         0.6700           PW         260         LLOCAMINI         335         10         0.0004         0.0001         0.6700           PW         260         LLCAFILL         336         1         0.0004         0.0004         0.0004           PW	18	젒	534	LAFSYMDDVV	320	10	0.0003				
PCL         515         LADGTSAIL         322         8           PCL         514         LADGTSAICS         322         11           PCL         514         LADGTSAICS         323         11         0.0025           PCL         514         LADGTSAICS         325         8         0.1000         0.2700         3.7000         0.2660           BW         251         LLCLFLLV         329         9         0.0034         3.7000         0.2660           BW         251         LLCLFLLVL         329         9         0.0034         3.7000         0.2660           BW         251         LLCLFLLVL         329         1         0.0013         0.0073         0.0073           BW         251         LLCLFLLVL         330         11         0.0013         0.0010         0.5700         0.5700           PW         250         LLDYCSAM         332         18         0.0014         0.0014         0.0014           PW         260         LLDYCSAM         332         1         0.0014         0.0014         0.5700         0.5700           PW         260         LLDYCSAM         332         1         0.0014         0.0014	18	젍	534	LAFSYMDDVVL	321	=					
PCL         515         LADOFTSANGSV         323         11           PCL         514         LLADOFTSANGSV         323         11           PCL         514         LLADOFTSAN         325         9         0.1000         0.2700         3.7000         0.26600           PCL         514         LLADOFTSAN         326         9         0.10075         3.7000         0.26600           BW         251         LLCLIFLLUL         329         10         0.0015         3.7000         0.26000           BW         251         LLCLIFLLUL         330         11         0.0015         0.0011           NC         30         LLOFARAT         333         10         0.0011         0.0200         0.5700           PW         260         LLOFARAPT         333         10         0.0011         0.0001         0.0000           PW         260         LLCFARAPT         335         1         0.0006         0.0000         0.5700           PCL         732         LLCAGAMWIN         334         9         0.0001         0.0006         0.0006           PW         250         LLICHELLUL         335         1         0.0006         0.0006	19	젍	515	LAQFTSAI	322	&					
BW         254         LILAGFISA         324         8         0.0025           POL         514         LILAGFISA         325         8         0.1000         0.2700         3.7000         0.2800           PAL         514         LILAGFISA         326         9         0.1004         0.2700         3.7000         0.2800           BW         251         LICUFILL         329         10         0.0013         0.0044           BW         251         LICUFILL         330         11         0.0013         0.0004           BW         251         LICUFILL         330         11         0.0013         0.0004           BW         250         LICOFANIM         332         8         0.0014         0.0004           PCL         752         LICCAMIN         334         10         0.0014         0.0004           PCL         752         LICCAMIN         335         1         0.0004         0.0010         0.0000           PCL         752         LICCAMIN         335         1         0.0004         0.0010         0.0000           PW         530         LILCIPELL         336         1         0.0004         0.0010	19	젍	515	LAQFTSAICSV	323	=					
PCL         514         LLAOFTSA         325         8         0.1000         0.2700         3.7000         0.2800           BW         251         LLCAFLAL         326         9         0.00048         9         0.00048           BW         251         LLCAFLAL         329         10         0.00059         9         0.00048           BW         251         LLCAFLAL         339         10         0.00059         9         0.00064           BW         251         LLCAFLAFT         332         10         0.00054         0.05700         0.5700           BW         260         LLDYSAL         332         10         0.00064         0.00064         0.00064         0.00064           POL         752         LLGCAAWWI         332         10         0.0016         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00066         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064         0.00064	20	8	254	LIFLIVLL	324	80	0.0025				
PCL         514         LLAGFTSAI         326         9         0.1000         0.2700         3.7000         0.2600           BW         251         LLCLFLLV         327         8         0.00048         3.7000         0.2600           BW         251         LLCLFLLVL         329         10         0.0075         8         0.00048           BW         251         LLCLFLLVL         330         11         0.0013         8         0.00044           BW         251         LLCLFLLVL         332         10         0.0016         0.0200         0.5700           BW         260         LLDCAANWI         332         10         0.0011         0.02200         0.5700           PCL         752         LLGCAANWI         333         10         0.0011         0.02200         0.5700           PCL         752         LLGCAANWI         334         9         0.0016         0.0016         0.5700           PCL         752         LLGCAANWI         335         9         0.0016         0.0016         0.5700         0.5700           BW         63         LLGNSPOA         334         1         1         0.0056         0.0016         0.0016<	19	젒	514	LLAGFTSA	325	<b>&amp;</b>					
BW         251         LICUFIL         327         8         0,0004           BW         251         LICUFILL         329         9         0,00075           BW         251         LICUFILL         330         11         0,0013           NDC         30         LICOFALL         330         11         0,0013           BW         260         LIDOSAME         332         10         0,0011         0,0001           PCL         752         LICCAANWIL         333         10         0,0011         0,0001           PCL         752         LICCAANWIL         335         10         0,0011         0,0001           PCL         752         LICCAANWIL         335         10         0,0014         0,0001           PCL         752         LICCAANWIL         335         11         0,0014         0,0001           PCL         752         LICCAANWIL         335         11         0,0018         0,0001           BW         63         LICKAANIC         336         1         0,0008         0,0009           BW         250         LICLICIAL         34         1         0,0008         0,0008           BW	19	전	514	LLAQFTSAI	326	6	0.1000	0.2700	3.7000	0.2600	0.7900
BW         251         LICUFLUL         328         9         0.0046           BW         251         LICIFLUL         329         10         0.0075           BW         251         LICIFLUL         329         10         0.0075           BW         260         LIDYGAML         333         10         0.0080         0.0001           BW         260         LIDYGAMW         333         10         0.0088         0.0001         0.0070           PCL         752         LIGCAMW         334         9         0.0011         0.0001         0.0000           PCL         628         LIGCAMW         334         9         0.0011         0.0000         0.6700           PCL         628         LIGCAMW         335         10         0.0014         0.0020         0.6700           PCL         628         LIGCAMW         337         8         0.0014         0.0020         0.6700           BW         63         LIGKAPOA         337         8         0.0006         0.0006         0.6700           BW         250         LICLEILL         34         1         0.0005         0.0005           BW         250	20	8	251	LICLIFIL	327	80	0.0004				
BW         251         LICLIFLUL         329         10         0.0075           NC         251         LICLIFLUL         330         11         0.0013           NC         260         LLDYOGAL         332         19         0.0004           POL         752         LLGCAANMI         333         10         0.0011           POL         752         LLGCAANMI         335         10         0.0014           POL         752         LLGCAANMI         335         10         0.0014           POL         752         LLGCAANMI         335         10         0.0016           BW         6.3         LLGWSPARFT         336         9         0.0016           BW         2.50         LLCIFLIA         34         11         0.0066           BW         2.50         LLCIFLIA         34         1         0.0066           BW         2.50         LLCIFLIA         34         1         0.0066           BW         2.50         LLCIFLIA         34         1         0.0066           BW         2.50         LLCIFLLA         34         1         0.0066           BW         2.50         LLCIFLLA <td>20</td> <td>8</td> <td>251</td> <td>LLCLIFLLV</td> <td>328</td> <td></td> <td>0.0048</td> <td></td> <td></td> <td></td> <td></td>	20	8	251	LLCLIFLLV	328		0.0048				
BW         251         LICLIFLUAL         330         11         0.0013           MAC         30         LICLIFLUAL         331         8         0.0004         0.0200         0.6700           BW         260         LIDYGAMLPM         333         10         0.0980         0.0001         0.0200         0.6700           PQL         752         LIGCAANWI         335         10         0.0014         0.0001         0.0001         0.0000         0.6700         0.6700           PQL         752         LIGCAANWI         335         10         0.0014         0.0001         0.0001         0.0001         0.0001         0.6700         0.6700           PQL         628         LIGCAANWI         335         11         0.0006         0.0001         0.0006         0.0001         0.0006         <	20	<b>№</b>	251	LICHELIVE	329	9 0	0.0075				
NJC         30         LLDTASAL         331         8           BW         260         LLDYGAML         332         8         0.0004         0.0200         0.6700           PQL         752         LLGCAANWI         333         10         0.0011         0.0001         0.0001         0.0000         0.6700         0.6700           PQL         752         LLGCAANWI         335         10         0.0011         0.0008         0.0001         0.0000         0.6700         0.6700           PQL         63         LLGKPADAPT         335         1         0.0008         0.0008         0.0008         0.0008         0.0008         0.0008         0.0008         0.0008         0.0008         0.0000	50	<u></u>	251	LICHELIVIL	330	2 =	0.0013				
BW         260         LIDYCGML         332         8         0.0004           POL         752         LLGCAANWI         333         10         0.0980         0.0001         0.6700           POL         752         LLGCAANWI         333         10         0.0140         0.0001         0.0700           POL         752         LLGCAANWI         335         10         0.0140         0.0008           POL         628         LLGCAANWI         335         10         0.0008         0.0008           BW         63         LLGWSPQAA         337         8         0.0006         0.0008           BW         250         LLCLIFIL         340         9         0.0006         0.0006           BW         250         LLCJFLLV         341         10         0.0005         0.0006           BW         250         LLCJFLLV         342         11         0.0005         0.0150         0.01006           BW         250         LLCJFLLV         343         8         0.0005         0.0106         0.0150           BW         250         LLCJFLLV         344         10         0.0026         0.0106           POL	17	S	30	LIDTASAL	331	∵ oc					
BW         260         LIDYGGMLPV         333         10         0.0380         0.0001         0.0200         0.6700           PQL         752         LICGAANWII         334         9         0.0011         0.0200         0.6700           PQL         628         LIGCAANWII         336         9         0.0008         0.0008           BW         63         LIGNSPOACSI         338         11         0.0006         0.0006           BW         250         LLICUFILVI         340         9         0.0005         0.0005           BW         250         LLICUFILVI         341         10         0.0005         0.0005           BW         250         LLICUFILVI         342         11         0.0005         0.0005           BW         250         LLICUFILVI         343         8         0.0005         0.0005           BW         250         LLICUFILVI         342         11         0.0005         0.0005           BW         250         LLICUFILVI         345         8         0.0005         0.0005           BW         378         LIPICALITY         345         8         0.0016         0.0150         0.2700      <	6	2	260	LIDYOGM	332	, α	0 0004				
POL         752         LIGCAANWIL         334         9         0.0011           POL         752         LIGCAANWIL         335         10         0.00140           POL         752         LIGCAANWIL         335         10         0.00140           BW         63         LIGWSPOACGI         336         9         0.00160           BW         63         LIGWSPOACGI         339         8         0.0006           BW         250         LLICLIFL         340         9         0.0006           BW         250         LLICLIFL         341         10         0.0006           BW         250         LLICLIFL         342         11         0.0006           BW         250         LLICLIFL         342         11         0.0005           BW         250         LLICLIFL         343         8         0.0110         0.0150         0.8000           POL         407         LLSSMLSWL         346         9         0.0110         0.0780         0.0150         0.8000           POL         407         LLSSMLSWL         345         8         0.0110         0.0780         0.0150           POL         407	8	<u></u>	260	LLDYOGMLPV	333	, <u>-</u>	0.0980	0 00 0	0000	0.6700	0000
POL         752         LIGCAANWIL         335         10         0.0140           POL         628         LIGKAAPFT         336         9         0.0008           BW         63         LIGKAAPFT         336         9         0.0006           BW         63         LIGKAPPT         339         8         0.0006           BW         250         LILCUFL         340         9         0.0065           BW         250         LILCUFLU         341         10         0.0036           BW         250         LILCUFLUL         343         8         0.0055           BW         270         LILCUFLUL         343         1         0.0005           BW         270         LILCUFLUL         343         8         0.0110         0.0150         0.8000           BW         270         LILCUFLUL         345         8         0.0110         0.0780         0.0150         0.8000           PCL         407         LLSNILSML         345         8         0.0110         0.0780         0.0150         0.2700           PCL         407         LLSNILSMLSMLSIL         345         8         0.0110         0.0780         0.0150<	9	<u></u>	752	LLGCAANWI	334	) o	0.0011	) ) )		9	0.0
POL         628         LIGFAAPFT         336         9         0.0008           BW         63         LIGWSPOA         337         8         0.0006           BW         250         LILCLIFL         349         9         0.0065           BW         250         LILCLIFLLV         341         10         0.0036           BW         250         LILCLIFLLV         343         8         0.0036           BW         250         LILCLIFLLV         343         8         0.0035           BW         250         LILCLIFLLV         343         8         0.0035           BW         378         LIPIFFCLWV         344         10         0.0320         0.0150         0.8000           POL         407         LISSINLSML         345         8         0.0110         0.0780         0.2700           POL         407         LISSINLSML         347         11         0.0026         0.0008         0.0150         0.2700           POL         407         LISSINLSML         349         8         0.0110         0.0780         0.2700           POL         407         LISSINLSML         349         8         0.0110	16	점	752	LLGCAANWIL	335	0	0.0140				
BNV         63         LIGWSPOAG         337         8           BNV         63         LIGWSPOAGG         338         11           BNV         250         LLLCLIFL         340         9         0.0065           BNV         250         LLLCLIFLLVL         341         10         0.0036           BNV         250         LLCLIFLLVL         342         11         0.0065           BNV         250         LLCLIFLLVL         343         8         0.0055           BNV         250         LLCLIFLLVL         344         10         0.0056           BNV         250         LLCIFLLVL         346         8         0.0110         0.0150         0.8000           POL         407         LLSNILSWLS         346         8         0.0110         0.0760         3.9000         0.2700           POL         407         LLSNILSWLS         347         11         0.0026         3.9000         0.2700           POL         436         LLVLDYOGAM         350         10         0.0056         3.9000         0.2700           BN         175         LLVLDYOGAM         351         11         0.0056         0.0056         0.0056	19	점	628	LLGFAAPFT	336	' თ	0.0008				
BNV         63         LLGUIFL         338         11           BNV         250         LLCLIFLL         339         8         0.0006           BNV         250         LLCLIFLLV         341         10         0.0005           BNV         378         LLPIFFCL         342         11         0.0005           BNV         378         LLPIFFCL         343         8         0.0110         0.0150         0.8000           POL         407         LLSGHH         345         8         0.0110         0.0780         0.2700           POL         407         LLSSNLSWL         346         9         0.0110         0.0780         0.2700           POL         407         LLSSNLSWL         346         9         0.0110         0.0780         0.2700           POL         407         LLSNLSWLSWL         346         9         0.0110         0.0780         0.2700           POL         436         LLYBILTI         348         8         0.0110         0.0780         0.2700           BN         155         LLVLDYOGAP         350         10         0.0310         0.0050         0.1500           BN         175         LV	17	8	63	LGWSPOA	337	- ∞					
BW         250         LLLCLIFL         339         8         0.0006           BW         250         LLLCLIFLL         340         9         0.0065           BW         250         LLLCLIFLLV         342         11         0.0055           BW         378         LLPFFCL         343         10         0.0320         0.0150         0.0800           BW         378         LLPFFCLW         345         8         0.0320         0.0106         0.0150         0.0800           POL         563         LLSMISML         345         8         0.0110         0.0320         0.0150         0.0800           POL         407         LLSSNISML         346         9         0.0110         0.0780         3.9000         0.2700           POL         407         LLSSNISMLS         347         11         0.0026         3.9000         0.2700           POL         436         LLYGSGL         349         8         0.0010         0.0780         0.0780           BW         257         LLVLDYCGML         350         10         0.0050         10         0.0074         0.0044           BW         175         LLVLOAGFFL         352	15	8	63	LLGWSPQAQGI	338	=					
BW         250         LLLCLIFLL         340         9         0.0065           BW         250         LLLCLIFLLV         341         10         0.0036           BW         378         LLLCLIFLLV         342         11         0.0055           BW         378         LLPFCL         343         8         0.0055           BW         378         LLPFCL         344         10         0.0320         0.0150         0.8000           POL         407         LLSNLSML         346         8         0.0110         0.0780         3.9000         0.2700           POL         407         LLSNLSMLSL         347         11         0.0016         3.9000         0.2700           POL         407         LLSNLSMLSL         349         8         0.0110         0.0780         3.9000         0.2700           POL         407         LLSNLSMLSL         349         8         0.0110         0.0780         0.0150         0.2700           POL         436         LLVLSSSGL         349         8         0.0026         0.0045         0.1500           BW         15         LLVLDAGFFL         352         10         0.0074         0.0074	20	8	250	LLICLIFL	339	8	0.0006				
BN         250         LILCUFILLY         341         10         0.0005           BN         250         LILCUFILLY         342         11         0.0005           BN         378         LIPFFCL         344         10         0.0320         0.0150         0.8000           POL         407         LISSNISMLSML         345         8         0.0110         0.0780         0.0150         0.8000           POL         407         LISSNISMLSML         346         9         0.0110         0.0780         3.9000         0.2700           POL         407         LISSNISMLSML         349         8         0.0016         0.0780         0.2700           POL         407         LISSNISMLSML         349         8         0.0026         3.9000         0.2700           POL         407         LISSNISMLSML         349         8         0.0026         3.9000         0.2700           BW         184         LITRILTI         349         8         0.0056         0.0002         0.0045         0.1500           BW         175         LIVLOAGEFIL         352         10         0.0074         0.0074         0.0045         0.0100           NC	20	8	250	LLICLIFIL	340	6	0.0065				
BW         250         LLLCLIFLLVL         342         11         0.00055           BW         378         LLPIFFCL         343         8         0.0055           BW         378         LLPIFFCLWV         344         10         0.0320         0.0150         0.8000           POL         563         LLSIGHL         345         8         0.0110         0.0780         0.0150         0.8000           POL         407         LLSNLSMLSMLS         346         9         0.0110         0.0780         3.9000         0.2700           POL         407         LLSNLSMLSMLS         347         11         0.0026         3.9000         0.2700           POL         436         LLSNLSMLSMLS         348         8         0.0026         3.9000         0.2700           POL         436         LLSNLSMLSMLS         349         8         0.0026         3.9000         0.2700           BW         175         LLVLDYGGML         350         10         0.0037         0.0045         0.1500           BW         175         LLVLOAGFFL         352         10         0.0770         0.0045         0.0100           NLC         100         LLWHHISCL	20	8	250	LLICLIFILV	341	10	0.0036				
BNV         378         LLPIFFCL         343         8         0.0055           BNV         378         LLPIFFCLWV         344         10         0.0320         0.0008         0.0150         0.8000           POL         563         LLSLGIHL         345         8         0.0110         0.0780         3.9000         0.2700           POL         407         LLSNLSML         346         9         0.0110         0.0780         3.9000         0.2700           POL         407         LLSNLSMLSL         347         11         0.0026         3.9000         0.2700           POL         407         LLSNLSMLSL         349         8         0.0026         3.9000         0.2700           BW         136         LLVGSSGL         349         8         0.0056         0.0056         0.0056           BW         175         LLVLDAGGFL         350         10         0.0050         0.0045         0.1500           BW         175         LLVLDAGGFL         354         10         0.0074         0.0042         0.0042           BW         175         LLVFHYOUR         355         9         0.0130         0.0042         0.0420 <t< td=""><td>20</td><td>2</td><td>250</td><td>LLICUFILM</td><td>342</td><td>=</td><td>0.0005</td><td></td><td></td><td></td><td></td></t<>	20	2	250	LLICUFILM	342	=	0.0005				
BW         378         LLPIFFCLWV         344         10         0.0320         0.0150         0.8000           POL         563         LLSCIHL         345         8         0.0110         0.0780         3.9000         0.2700           POL         407         LLSSNLSWLS         346         9         0.0110         0.0780         3.9000         0.2700           POL         407         LLSSNLSWLS         347         11         0.0026         3.9000         0.2700           POL         407         LLSSNLSWLS         348         8         0.0026         3.9000         0.2700           BW         184         LLTRILTI         349         8         0.0026         3.9000         0.2700           BW         257         LLVLLDYGAM         351         11         0.0050         0.0045         0.1500           BW         175         LLVLOAGFFL         352         10         0.0074         0.0045         0.1500           BW         175         LLWFHISCL         354         10         0.0130         0.0042         0.0420         0.3100           NC         100         LLWFHISCLT         356         9         0.0130         0.0042	50	8	378	LLPIFFOL	343	80	0.0055				
POL.         563         LLSLGIHL         345         8           POL.         407         LLSSNLSWL         346         9         0.0110         0.0780         3.9000         0.2700           POL.         407         LLSSNLSWLSL         346         9         0.0110         0.0780         3.9000         0.2700           POL.         407         LLSSNLSWLSL         347         11         0.0026         3.9000         0.2700           BN         184         LLTRILTI         349         8         0.0026         3.9000         0.2700           BN         257         LLVLDYGGML         350         10         0.0050         3.9000         0.1500           BN         175         LLVLDYGGML         351         11         0.0050         0.0045         0.1500           BN         175         LLVLQAGFFL         353         11         0.0074         0.0045         0.1500           BN         175         LLVLQAGFFL         354         10         0.6700         0.3800         1.7000         0.2900           NC         100         LLWFHISCLT         356         9         0.0130         0.0042         0.0420         0.3100	20	8	378	LLPIFFCLWV	344	10	0.0320	0.0008	0.0150	0.8000	0.0005
POL.         407         LLSSNLSWL         346         9         0.0110         0.0780         3.9000         0.2700           POL.         407         LLSSNLSWLSL         347         11         0.0026         3.9000         0.2700           BN         184         LLTRILT1         348         8         0.0026         0.0026           POL.         436         LLVGSSGL         349         8         0.0050         0.0050           BN         257         LLVLDYOGML         351         11         0.0050         0.0045         0.1500           BN         175         LLVLOAGFFL         352         10         0.0074         0.0045         0.1500           BN         175         LLVLOAGFFL         353         11         0.0074         0.0045         0.1500           BN         175         LLVLOAGFFL         354         10         0.6700         0.3800         1.7000         0.2900           NLC         100         LLWFHISCL         355         9         0.0130         0.00420         0.0420         0.3100           NLC         100         LLWFHISCL         356         9         0.0130         0.00420         0.0420         0.3100 <td>19</td> <td>쩝</td> <td>563</td> <td>LLSLGIHL</td> <td>345</td> <td>œ</td> <td></td> <td></td> <td></td> <td></td> <td></td>	19	쩝	563	LLSLGIHL	345	œ					
POL.         407         LLSSNLSWLSL         347         11           BN         184         LLTRILTI         348         8         0.0026           POL.         436         LLVGSSGL         349         8         0.0050           BN         257         LLVLDYGGML         351         11         0.0037         0.0045         0.1500           BN         175         LLVLOAGFFL         352         10         0.0074         0.0045         0.1500           BN         175         LLVLOAGFFL         353         11         0.0074         0.0045         0.1500           BN         175         LLVLOAGFFL         353         11         0.0074         0.0045         0.1500           NLC         100         LLWFHISCL         354         10         0.6700         0.3800         1.7000         0.2900           NLC         100         LLWFHISCL         356         9         0.0130         0.00420         0.0100           NLC         100         LLWFHISCL         356         9         0.0130         0.00420         0.0420         0.3100           POL         643         LMPLYACI         357         8         8	18	점	407	LLSSNLSWL	346	თ	0.0110	0.0780	3.9000	0.2700	0.0100
BN         184         LLTRILTI         348         8         0.0026           POL         436         LLVGSSGL         349         8         0.0050           BN         257         LLVLDYGGML         351         11         0.0037         0.0045         0.1500           BN         175         LLVLQAGFFL         352         10         0.0074         0.0045         0.1500           BN         175         LLVLQAGFFL         353         11         0.0074         0.0004         0.1500           BN         175         LLVLQAGFFL         354         10         0.6700         0.3800         1.7000         0.2900           NLC         100         LLWFHISCL         355         9         0.0130         0.0022         0.0420         0.3100           NLC         100         LLWFHISCL         356         8         0.0130         0.00420         0.3100           POL         643         LMPLYACI         357         8         8         8	18	전	407	LLSSNLSWLSL	347	=					
POL.         436         LLVGSSGL         349         8           BN         257         LLVLDYGGML         350         10         0.0050           BN         257         LLVLDYGGML         351         11         0.0310         0.0045         0.1500           BN         175         LLVLQAGFFL         352         10         0.0074         0.0045         0.1500           BN         175         LLVLQAGFFL         353         11         0.0074         0.0007         0.2900           NLC         100         LLWFHISCL         354         10         0.6700         0.3800         1.7000         0.2900           NLC         100         LLWFHISCL         356         9         0.0130         0.0022         0.0420         0.3100           POL         643         LMPLYACI         357         8           BN         178         LQAGFFL         358         8	16	8	184	LLTRILTI	348	80	0.0026				
BN         257         LLVLDYGGM         350         10         0.0050           BN         257         LLVLDYGGML         351         11         0.0310         0.0045         0.1500           BN         175         LLVLQAGFFL         352         10         0.0074         0.0045         0.1500           BN         175         LLVLQAGFFL         353         11         0.0074         0.0002         0.1500           BN         338         LLVPFVQWFV         354         10         0.6700         0.3800         1.7000         0.2900           NLC         100         LLWFHISCL         355         9         0.0130         0.0022         0.0420         0.3100           NLC         100         LLWFHISCL         356         9         0.0130         0.0002         0.0420         0.3100           POL         643         LMPLYACI         8         8         8         8	16	절	436	LLVGSSGL	349	80					
BN         257         LLVLDYQGML         351         11         0.0310         0.0045         0.1500           BN         175         LLVLQAGFFL         352         10         0.0074         0.0045         0.1500           BN         175         LLVLQAGFFL         353         11         0.0074         0.2900           BN         338         LLVPFVQWFV         354         10         0.6700         0.3800         1.7000         0.2900           NLC         100         LLWFHISCL         355         9         0.0130         0.0022         0.0420         0.3100           NLC         100         LLWFHISCLT         356         10         8         8           POL         643         LMPLYACI         358         8	19	<b>≥</b>	257	птипруосу	350	10	0.0050				
BN         175         LLVLQAGFFL         352         10         0.0310         0.0045         0.1500           BN         175         LLVLQAGFFL         353         11         0.0074         0.0074         0.2900           BN         338         LLVPFVQWFV         354         10         0.6700         0.3800         1.7000         0.2900           NLC         100         LLWFHISCL         355         9         0.0130         0.0022         0.0420         0.3100           NLC         100         LLWFHISCLT         356         10         0.0130         0.0002         0.0420         0.3100           POL         643         LMPLYACI         357         8         8         BW         178         LQAGFFL         358         8	19	2	257	LLVLLDYOGML	351	Ξ					
BN         175         LLVLQAGFFLL         353         11         0.0074           BN         338         LLVPFVQWFV         354         10         0.6700         0.3800         1.7000         0.2900           NLC         100         LLWFHISCL         355         9         0.0130         0.0002         0.0420         0.3100           NLC         100         LLWFHISCL         356         10         310         310           POL         643         LMPLYACI         357         8         8           BW         178         LQAGFFL         358         8	<del>1</del> 8	2	175	LLVLQAGFFL	352	10	0.0310	0.0037	0.0045	0.1500	0.0110
BN         338         LLVPFVQWFV         354         10         0.6700         0.3800         1.7000         0.2900           NLC         100         LLWFHISCL         355         9         0.0130         0.0002         0.0420         0.3100           NLC         100         LLWFHISCLT         356         10         0.0130         0.0002         0.0420         0.3100           POL         643         LMPLYACI         357         8         8           BN         178         LQAGFFL         358         8	<del>-</del>	<u>8</u>	175	LLVLQAGFFLL	353		0.0074				
NUC 100 LLWFHISCL 355 9 0.0130 0.0002 0.0420 0.3100  NUC 100 LLWFHISCLT 356 10  POL 643 LMPLYACI 357 8  BW 178 LQAGFFL 358 8	19	8	338	LLVPFVQWFV	354	10	0.6700	0.3800	1.7000	0.2900	0.1400
NUC 100 LLWFHISCLT 356 POL 643 LMPLYACI 357 BW 178 LQAGFFL 358	18	3	100	LLWFHISOL	355	თ	0.0130	0.0002	0.0420	0.3100	0.0098
POL 643 LMPLYACI 357 BW 178 LQAGFFL 358	17	3	100	LLWFHISCLT	356	10					
BN 178 LOAGFFL 358	19	전	643	LMPLYACI	357	80					
	19	8	178	LOAGERI	358	α					

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Table VIII	=			HBV A02 SU	A02 SUPER MOTIF (With binding information	(With bindi	ng informa	tion)			
rservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A-0201	A.0202	. A*0203	A*0206	A.6802
56	1.9	¥.	178	LOAGEFIT	359	σ					
80	9 1	; }	178	LOAGFFLLTRI	360	· =					
100	20	점	401	LOSLTNIL	361	80					
92	19	3	108	LTFGRETV	362	80					
7.5	15	3	137	LTFGRETVL	363	o					
06	18	점	404	LTNLLSSNL	364	6					
80	16	<u>8</u>	185	LTRILTIPOSL	365	=					
85	17	절	66	LTVNEKRRL	366	6					
100	20	절	364	LVDKNPHNT	367	6	0.0001				
92	19	8	258	LVLLDYGGM	368	თ	0.0001				
92	19	2	258	LVLLDYQGML	369	10	0.0001				
90	18	<b>&amp;</b>	176	LVLOAGFFL	370	6	9600.0				
06	18	8	176	LVLQAGFFLL	371	10	0.0022				
06	18	8	176	LVLQAGFFLLT	372	Ξ					
92	19	8	339	LVPFVQWFV	373	6	0.0420	0.0150	0.0048	0.7900	2.8000
95	19	8	339	LVPFVQWFVGL	374	=					
90	18	3	119	LVSFGVWI	375	œ	0.0004				
90	18	3	119	LVSFGVWIRT	376	10					
85	17	<b>}</b>	360	MMWYWGPSL	377	6	0.6400				
7.5	15	3	-	MOLFHLCL	378	æ					
100	20	2	136	NAPILSTL	379	æ					
100	20	3	136	NAPILSTLPET	380	Ξ					
92	19	점	42	NLGNLNVSI	381	6	0.0047				
06	<del>. 1</del>	절	406	NLLSSNLSWL	382	10	0.0016				
98	19	젍	45	NLNVSIPWT	383	6	0.0005				
100	20	전	400	NLOSLTNL	384	æ					
100	20	젗	400	NLOSLTNLL	385	თ	0.0047				
75	15	8	15	NLSVPNPL	386	œ					
06	18	점	411	NLSWLSLDV	387	6	0.0650	0.0051	0.6400	0.1600	0.0990
06	18	점	411	NLSWLSLDVSA	388	Ξ					
100	20	점	47	NVSIPWTHKV	389	10	0.0001				
100	20	전	430	PAAMPHLL	390	89					
85	17	점	430	PAAMPHLLV	391	o					
90	18	점	775	PADDPSRGRL	392	10					
90	18	8	131	PAGGSSSGT	393	တ					
90	18	8	131	PAGGSSSGTV	394	01					
92	19	점	641	PALMPLYA	395	æ					
92	19	점	641	PALMPLYACI	396	10	0.0001				
7.5	15	×	145	PAPCNFFT	397	ω					
7.5	15	×	145	PAPCNFFTSA	398	10					
80	16	×	Ξ	PARDVLCL	399	œ					
7.5	15	×	=	PARDVLCLRPV	400	=					

	=			NO ANA OLI		-	•				
onservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	AA	A*0201	A.0202	A*0203	A.0206	A.6802
06	18	\$	355	PARVTGGV	401	8					
90	18	점	355	PARVTGGVFL	402	. 10					
06	18	전	355	PARVTGGVFLV	403	=					
92	19	3	130	PAYRPPNA	404	80					
95	19	3	130	PAYRPPNAPI	405	10	0.0001				
95	19	3	130	PAYRPPNAPIL	406	Ξ					
85	17	점	616	PIDWKVCQRI	407	10	0.0001				
85	17	전	616	PIDWKVCORIV	408	1					
100	20	8	380	PIFFCLWV	409	80	-				
100	. 02	8	380	PIFFCLWVYI	410	10	0.0004				
82	17	젍	713	PIHTAELL	411	80					
82	17	점	713	PIHTAELLA	412	6					
85	17	전	713	PIHTAELLAA	413	10					
80	16	젗	496	PIILGFRKI	414	6	0.0001				
80	16	전	496	PIILGFRKIPM	415	Ξ					
100	20	3	138	PILSTLPET	416	O	0.0001		•		
100	20	3	138	PILSTLPETT	417	10	0.0001				
100	20	3	138	PILSTLPETTV	418	=	0.0001				
80	16	8	314	PIPSSWAFA	419	6					
95	19	ಕ್ಷ	20	PLEEELPRL	420	6	0.0003				
06	18	ದ್ದ	20	PLEEELPRIJA	421	10	0.0001				
92	19	<b>}</b>	10	PLGFFPDHOL	422	10	0.0002				
100	20	젇	427	PLHPAAMPHL	423	10	0.0001				
100	20	ರ	427	PLHPAAMPHLL	424						
100	20	8	377	PLLPIFFCL	425	6	0.0650	0.0001	0.0018	0.1100	0.0047
100	20	<b>}</b>	377	PLLPIFFCLWV	426	=					
06	18	2	174	PLLVLQAGFFL	427	=	0.0008				
80	16	젗	711	PLPIHTAEL	428	6	0.0004				
80	16	젗	711	PLPIHTAELL	429	0	0.0001				
80	16	전	711	PLPIHTAELLA	430	Ξ					
75	15	전	۲	PLSYOHFTIKL	431	10	0.0001				
75	15	전	5	PLSYQHFPKLL	432	Ξ					
85	17	전	98	PLTVNEKRRL	433	10	0.0001				
80	16	전	202	PMGVGLSPFL	434	10	0.0001				
80	16	전	505	PMGVGLSPFIL	435	=					
95	19	2	106	POAMOWNST	436	თ					
80	16	<b>}</b>	106	POAMOWNSTT	437	10					
06	18	<b>}</b>	192	POSLDSWWT	438	თ					
06	18	2	192	POSLDSWWTSL	439	Ξ					
75	15	절	692	PTGWGLAI	440	<b>co</b>					
80	16	2	219	PTSNHSPT	441	80					
82	17	ದ	797	PTTGRTSL	442	œ					

	A.6802																																								
٠	A.0206																																								
	A*0203		•																																						
tion)	A.0202																																								
ng informa	A.0201							0.0002										0.0001	0.0001	0.0001	0900.0		0.0001		0.0010	•												0.0001			0.0041
(With bindi	AA	10	80	01	80	10	8	10	80	=	∞ ∶	o ;	= «	o Ç	2 a	o	10		<b>o</b>	1	. 01	11	6	<b>&amp;</b>	o	o	10	<b>∞</b> ∶	10	_ •	• ‡	_ α	0 0 0 0	=	σο.	=	80	10	=	80	6
SUPER MOTIF (With binding information)	SEQ ID NO:	443	444	445	446	447	448	449	450	451	452	455 803	† u v	450	457	458	459	460	461	462	463	464	465	466	467	468	469	470	1 / 4	274	474	475	476	477	478	479	480	481	482	483	484
HBV A02 S	Sequence	PTTGRTSLYA	PTVQASKL	PTVQASKLCL	PTVWLSVI	PTVWLSVIWM	PVCAFSSA	PVNRPIDWKV	QAFTFSPT	QAFTESPTYKA		OAGEFIL IRI	מאטיינים מייט	CALCWGEL CAL CACELM	OAMOMNST	DAMOWNSTT	OASKLCLGWL	QLDPARDV	QLDPARDVL	QLDPARDVLCL.	OLLWFHISCL	QLLWFHISCLT		RAFPHCLA	RILTIPOSL	RIVGLLGFA	RIVGLLGFAA	RLKLIMPA	HOALCWGEL POTE CHOSTS	HCALLCWGELM POLIMONI	BOLIWERISC	ROSGROPT	RTPARVTGGV	RTPPAYRPPNA	RVAEDLNI.	RVAEDLNLGNL	RVHFASPL	RVHFASPLHV	RVHFASPLHVA	RVTGGVFL	RVTGGVFLV
	Position	797	15	15	351	351	29	612	654	654	179	179	2.5	) C	107	107	18	΄ ∞	80	80	66	66	685	528	187	624	624	106	3 0	٥ o	0 0	80	353	127	36	36	818	818	818	357	357
	Protein	정	3	3	8	<b>}</b>	×	전	전	전 	} ;	<b>}</b> ∂	<u>ک</u> ج	3 5	} €	<u>}</u>	2	×	×	×	3	2	텇	ಶ	8	점	ත් :	전 :	3 5	3 5	3 2	2	දූ	3	정	점	점	전	전	젒	젍
=	Frequency	17	16	16	15	15	19	17	19	6	19	<u>ه</u> د	D 9	0 0	o	9 -	91	16	16	16	18	17	19	19	16	18	18	5 .	80 9	0 0	o œ	17	. 81	19	19	18	16	15	15	20	20
Table VIII	Conservancy	85	80	80	7.5	7.5	92	82	95	95	95	ے د	9 6		, c	0 80	80	80	80	80	06	85	92	92	80	06	06	75	0.6	0 6	0 0	22.00	06	9.2	95	06	80	7.5	7.5	100	100

Table VIII	≡			HBV A02 SI	A02 SUPER MOTIF (With binding information)	(With bind	ng informa	ition)			
Conservancy	Frequency	Protein	Position	Sequence	SEQ ID NO:	АА	A-0201	A.0202	A-0203	A.0206	A.6802
0	α÷	>	2.5	SAGBCALBET	485	0 +					
9 4	o c	ς ζ	20.4	1 11 12 12 12 12 12 12 12 12 12 12 12 12	486	2 5	000				
S 6		3 2	35	SALVREAL	487	<u>?</u> α					
100	20	<u></u>	9 4	SIPWTHKV	488	o 00					
56	6 -		194	SLDSWWTSL	489	ာတ					
75	5 - 5	<u>ද</u>	565	SLGIHLNPNKT	490	· =					
5 6	19	8	337	SLLVPFVQWFV	491	Ξ	٠				
7.5	15	<u>ਵ</u>	581	SUNFMGYV	492	΄ ω					
7.5	15	절	581	SLNFMGYVI	493	6	0.0038				
95	. 19	×	54	SLRGLPVCA	494	o	0.0007				
06	18	절	403	SLTNLLSSNL	495	10	0.0014				
7.5	15	8	216	SOSPTSNHSPT	496	Ξ					
75	15	8	280	STGPCKTCT	497	6					
100	20	3	141	STLPETTV	498	ဆ					
100	20	3	141	STLPETTW	499	6	0.0019				
80	16	8	85	STINROSGROPT	200	Ξ					
85	17	젍	548	SVOHLESL	501	œ					
80	16	8	330	SVRFSWLSL	502	ത	0.0001				
80	16	8	330	SVRFSWLSLL	503	10	0.0004				
80	16	8	330	SVRFSWLSLLV	504	=					
90	18	젍	739	SVVLSRKYT	. 202	6					
95	19	ಕ	524	SWRRAFPHCL	506						
85	17	젍	716	TAELLAACFA	207	10					
95	19	3	53	TALROAIL	508	æ					
80	16	3	33	TASALYREA	509	ō					
. 80	16	3	33	TASALYREAL	510	10					
06	18	8	190	TIPOSLDSWWT	511	=					
100	20	3	142	TLPETTW	512	80					
100	20	전	150	TLWKAGIL	513	80					
98	19	전	989	TOCGYPAL	514	80					
95	19	점	636	TOCGYPALM	515	ō					
i 95	19	젍	636	TOCGYPALMPL	516	=					
85	17	젒	798	TTGRTSLYA	517	6					
7.5	15	2	278	TTSTGPCKŢ	518	6					
7.5	15	8	278	TTSTGPCKTCT	519	Ξ					
85	17	점	100	TVNEKRRL	520	ω					
80	16	3	16	TVQASKLCL	521	თ	0.0002				
7.5	15	8	352	TVWLSVIWM	522	თ	0.0002				
98	19	점	37	VAEDLNLGNL	523	10	0.0001				
95	19	×	15	. VLCLRPVGA	524	თ	0.0014				
85	17	점	543	VLGAKSVQHL	525	10	0.0001				
06	<del>1</del> 8	×	133	VLGGCRHKL	526	o	0.0009				

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Table VIII

A.6802				0.0002	0.0170																				0.0310								0.0320					0.0002				
A.0206				0.9000	0.3400																				0.3600								0.1000					0.1000				
A.0203				0.0210	4.9000																				7.2000								0.5600					0.0024				
A.0202				0.0001	0.2200																				0.0380								0.0005					0.0001				
A.0201	0.0001	0.0012		0.0440	0.5800	0.0019	0.0660	0.0011	•								0.0003		0.0270		0.0053			0.0059	1.1000		0.0005	0.0019	0.0009	0.0001			0.0160			0.3800		0.0250				
AA	10	6	80	o	=	∞	6	10	æ	Ξ	10	11	80	80	=	∞	10	=	6	11	10	11	80	6	6	89	თ	Ξ	0	6	=	80	10	-	80	6	-	6	10	80	6	10
SEQ ID NO:	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	260	561	562	563	564	565	266	267	568
Sequence	VLGGCRHIALV	VLHKRTLGL	VLLDYQGM	VLLDYGGML	VLLDYQGMLPV	VLOAGFFL	VLOAGFFLL	VLQAGFFILT	VOASKLCL	VOASKLCLGWL	VQWFVGLSPT	VQWFVGLSPTV	VTGGVPLV	VVLGAKSV	WLGAKSVQHL	WLSRKYT	WRRAFPHCL	VVRRAFPHCLA	WILRGTSFV	WILRGTSFVVV	WLLGCAANWI	WLLGCAANWIL	WLSLDVSA	WLSLDVSAA	WLSLLVPFV	WMCLRRFI	WMCLRRFII	WMCLRRFIIFL	WMMWWGPSL	WTHKVGNFT	WITHKVGNFTGL	YLHTLWKA	YLHTLWKAGI	YLHTLWKAGIL	YLPLDKGI	YLVSFGVWI	YLVSFGVWIRT	YMDDVVLGA	YOGMLPVCPL	YOHFRALL .	YOHFRALL	YOHFRKLLLL
Position	133	92	259	259	259	177	177	177	17	17	343	343	358	542	542	740	525	525	759	759	751	751	414	414	335	237	237	237	359	25	52	147	147	147	122	118	118	538	263		Ŋ	ហ
Protein	×	×	8	8	8	8	8	8	3	3	8	8	전	젒	전	점	점	점	정	Σ,	전	전	ಕ್ಷ	젙	}	8	8	<b>₩</b>	2	점	점	점	점	점	점	3	3	젙	<b>≥</b>	점	점	<u>Ğ</u>
Frequency	18	17	49	19	18	19	19	19	16	16	19	19	20	18	16	18	19	19	16	16	16	16	20	19	20	19	19	19	17	20	19	20	20	20	20	18	. 89	18	18	15	15	15
Conservancy Frequency Protein Position	06	85	95	95	06	95	98	95	80	80	95	95	100	06	80	06	95	95	80	80	80	80	100	95	100	95	95	95	85	100	95	100	100	100	100	06	06	90	06	7.5	7.5	7.5

Table VIII	<b>=</b>			HBV A02 SU	HBV A02 SUPER MOTIF (With binding information)	With binding	informa	tion)			
onservancy	onservancy Frequency Protein Position Sequence	Protein	Position	Sequence	SEQ ID NO:	АА	A*0201 A*0202	A.0202	A*0203	A.0206 A.6802	A-6802
85	17	절	746	YTSFPWLL	569	æ					
7.5	15	점	746	YTSFPWLLGCA	570	-					
06	18	젙	768	YVPSALNPA	571	6	0.0039				

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A03
HBV

·	SEQ ID NO:	572	574	575	576	578	579	580	581	582	584	585	586	28./ 688	283	290	591	592	593	595	596	597	200	009	601	602	500	605	909	607	808	610	611	612	613	0 0 0 0 0	616	617	618	6 C C	621	622
	A-6801	0.0014	0.000	0.0004	0	0.0001	0.7300		0.0440	0.0410	0.0110		0.1600	0.0027			0.0590		1.5000		0.0003		0.000.0	0.0001	0.6600			0.1900	0.0017	0.0001	0.000		0.0064			•	0.0078		0.0001	0 4900		0.0001
	A*3301	0.0035	6000.0-	0.0230	0	0.0008	8.0000		0.0250	3.7000	0.0015		0.2000	0.1400			0.2100	:	0.0350		0.000		-0.0009	-0.006	0.7300			0.0720	-0.0009	-0.0009	0170	2	0.0029				-0.0023		-0.0009	0 2300	2	-0.0009
	A-3101	0.0056	0.00	0.0450	0	0.0088	1.5000		0.0520	2100.0-	-0.0012		0.0200	-0.0009			0.0023		0.0170		0.0009		0.0009	-0.0002	6.8000			0.0370	0.0017	0.0015	0009	9	0.0015				-0.0012		-0.0009	0.0260		-0.0009
nation)	A-1101	0.0003	0.0003	0.0009		0.0002	0.0230	0.0001	0.0001	-0.0003	-0.0003	0.0004	0.0016	-0.0002	00.0		0.0100	0.0003	0.0092	0.0030	0.0011		0.0004	0.5600	0.1700	0.0065	6	0.4400	0.0002	-0.0002	0000	0.0065	0.0003	:	0.0002		0.0008		-0.0002	0.0120		-0.0002
ing inforn	A*0301	0.0004	0.0003	0.0047	0	0.0009	0.0034	0.0011	0.0029	0.0042	-0.000	0.0002		0.0003			0.0100	0.0003	0.0065	0.0430	0.0025		0.0006	0.0010	0.1900	0.0160	36000	0.5400	0.0004	0.0002	00.70	0.0058	0.0024	•	0.0050		-0.0009		-0.0002	0.0028	9	-0.0002
(With binding information	AA	= co c	o 0-	&	<b>თ</b> (	<b>ઝ</b> α	ით	10	σ,	Ξ α	· =	்	=	πο <del>ς</del>	0 0	0 0	&	10	Ξ,	ກວ	.01	Ξ,	∞ <del>,</del>		Ξ.	တပ	<b>x</b> 0 C	· =	∵ ∞	<b>∞</b> ;	٦ •	ກ່ວາ	80	0 :	₽;	= =	: <del>; :</del>	80	<b>&amp;</b>	љ <del>-</del>	2 =	ဆ
MOTIF	C- term	α: c	<b>c</b> cc	œ	œ	rα	: oc	Œ	œ	ra	: cc	œ	œ	<b>=</b> 0	c oc	: cc	×	æ	oc 3	< <u>×</u>	×	œ :	× 0	c 7	: cc	œ:	<b>∠</b> 0	<b>:</b> ¥	ac ac	ac :	<b>∠</b> 0	: ac	œς	<b>ac</b> 1	oc o	r ¥	: 00	¥	ac 0	r a	×	œ
SUPER	P2	∢-	د -	· _	တ	ი ∢	< ∢	_	<b>ω</b> .	<b>-</b>	- ∢		ا ب	- +	- ∢	ဗ	<b>-</b>	<b>-</b> 1	⊢ >	> _	_	<b>-</b> :	⊦≥	- J-	· >			J }-	တ	∢.	< ب	• «	_		<b>_</b> .	ى ر	တ	တ	⊢:	> >	• w	_
HBV A03 S	Sequence	AACFARSR	ALNPADDPSR	ALRFTSAR	ASPLHVAWR.	CAANWIIB	CALRFTSAR	CLRPVGAESR	CSPHHTALR	DLLDIASALYH DTASAI YB	EAGPLEEELPR	ELLAACFAR	ELLAACFARSR	CTTAMORRE	FASPI HVAWR	FSSAGPCALR	FTFSPTYK	FTSAICSVVR	FTSAICSWAR	GIFLNPNK	GIHLNPNKTK	GIHLNPNKTKR	GMDIDPYK	GTDNSWLSRK	GVWIRTPPAYR	HISCLIFGR	HINFAKIK	HTLWKAGILYK	ISCLIFGR	KAGILYKR	KLFVNHFIUWK	LAACFARSR	LLAACFAR	LLAACFARSR	LLDTASALYR	LEGCAANWILK 1 SI GIHI NPNK	LSTLPETTWR	LSYQHFRIX	LTVNEKRR	LVSPGVWIR	MSTTDLEAYFK	NLEDPASR !
	Position	721	321 772	70	822	84 755	69	17	8 6	5 C C	17	718	718	174	821	63	656	518	518	567	567	567	29	735	123	104	999 999	149	105	153	610	720	719	719	30	752	169	ო	66	911	103	75
	Protein	젍	ಕ ಕ	×	젍	≩ &	<u>.</u>	×	2 5	3 2	_ ಶ	ਲ	점 :	2 2	₹ 2	! ×	전	젍:	ಕ್ತ ,	< ই	ස්	호 :	Ş ⊊	<u> </u>	3	3	로	<u> </u>	3	덛 :	젇 >	ر کا	ਫ਼	젍	9 8	₹ <b>8</b>	3	젍	젍 :	3 8	<u></u> ×	3
	Frequency	17	° €	17	9 ;	င် ၃ န	12	18	50	- 1	- 6	18	17	9	9 4	<del>-</del> <del>-</del>	6	19	o .	- <del>-</del>	15	15	7	• <del>•</del>	0	8 :		50	18	20		- 1	18	17	17	٠ ٠	- <del>-</del> -	15	7	18	1.5	18
Table IX	Conservancy	85	c 0	85	80	8 80 80	8 62	06	100	20 ec	9 6	06	92	500	0 8	0 6	95	98	S 6	90	75	7.5	တ္ဆ	) ()	9 6	06	7.5	100	06	100	i 80 76		06	85	82	80	9 6	7.5	82	9 5 5 5	75	06

	SEQ ID NO:	623	624 625	626	627	628	629	631	632	633	634	635	636	938	639	640	641	642	643	644	645	646	647	040	650	651	652	653	654	655 656	657	658	629	099	661	200	664	665	999	299	899	699	0/0	672	673	
	.A*6801 S	0.0019	0.0007	0.0002	0.0002			0.0001	0.0001	0.0002	0.0001	0.0002	0.0002	1 2000	200			0.0002		6.1000	0.0003		0000	0.000	0.000	0.0360	0.0690	0.3800	0.0003	0.037.0	0.0250	0.3100			0.0590	0.0180	0.6400	0.0130	0.0640	0.0820	0.0048	0.0170	3000	0.0033		
	A*3301 .	-0.0023	0.0009	0.0015	0.0180			6000 0-	-0.0009	0.0008	-0.0009	0.0027	0.0043	0.0008				0.0490		1.2000	-0.0023		7	0.00	-0.0003	0.0024	0.0081	0.0650	-0.0023	1600	0.1000	0.1600			0.1600	0.0024	0.0710	0.0010	0.1100	0.0200	0.0066	0.0012	0	20.7		
	A.3101	-0.0012	-0.0009	0.0004	0.0100			600000-0-	-0.0009	9000.0	-0.0009	0.0004	0.0004	0.0002	2			3.1000		2.6000	0.0190		000	0.0033	-0 0002	0.0029	0.0280	0.1500	-0.0012	0 3300	0.3300	0.1000		0	0.0066	0.000	0.0061	0.0051	0.1000	0.0600		9000.0	0	0.63.0		
nation)	A-1101	0.0005	0.0010	0.0002	0.0002		0.0002	-0.0002	-0.0002	0.0031	-0.0002	0.0005	0.0005	0.5400				0.0002		3.8000	-0.0003		. 0	-0.0002	0.000	0.0020	0.0071	0.2100	-0.0003	0071	0.1400	1.4000		2.7000	0.0023	0.000	0.0160	0.3600	0.0095	0.0008		0.9200	4000	0.0003		•
g inforr	A-0301	-0.0009	0.0006	0.0008	0.0002	•	0.0002	0.0002	-0.0002	0.0011	0.0005	0.0008	0.0002	0.03	0.0			0.0950		0.2800	-0.0007		0	-0.0002	0.0034	-0.0002	-0.0002	0.0058	-0.0004	0000	0.0000	0.0150		0.0066	0.0006	00000	0.0005	5.3000	0.0082	0.0005	0.0018	0.0006	0	0.0003		
SUPER MOTIF (With binding information)																																														
F (With	AA	11	oo d	တ	6	은 (	<b>σ</b> ο α	0 00		6	æ ·	6	<b>о</b>	n <del>-</del>	<u>2</u> თ	· =	80	6	=	Ξ	=	<b>ω</b> (	on c	00	» <u>-</u>	. ao	80	6	Ξ ;	2 ∘	. <del>.</del>	=	60	<del>2</del> ;	Ξ <	n ⊊	= =	10	? =	6	9	<b>o</b> (	<b>20</b> C	,	Ξ	
MOTI	C. term	×	× ×	c oc	αc	<b>cc</b> (	<b>x</b> x	2 م	· œ	×	œ	<u>ac</u> 1	<b>x</b> >	<b>4</b> ×	2 00	<u>a</u>	œ	œ	Œ	Œ	œ	ac o	ac (	<b>c</b> 0	c ×	: ac	Œ	Œ	<b>c</b> :	∠ 0	c a	Œ	œ	× (	rc	ca	: oc	: <b>×</b>	œ	œ	œ	×	∠ 0	c ac	Œ	
UPER	P2	_	w >	• ∢	∢	∢ ·			ـ ا	_	. د	<b>_</b> :	> >	> <	< ∢	တ	တ	_	ب	ب	တ	တ (	S) F	- ⊦	- >	۰ «	∢	∢	∢ .	ں ر	o <b>-</b>	- 1-	<b>-</b>	۰ -	∢ -	ـ د	ب د	ـ ا	ىـ ،	တ	တ	<b>-</b>	- +	- >	>	
HBV A03 S	Sequence	NLNVSIPWTHK	NSVALSRK	PADDPSRGR	PARDVLCLR	PASTNROSGR	PIDWKVCCH PIII GEBK	ACTED NO.	PLSYCHER	PLSYCHFFIX	PLTWNEKR	PLTVNEKAR	PVGAESHGR	OAFTESPINK	OAGFRITE	OSPRARASOSR	OSSGILSR	RLKLIMPAR	RLKVFVLGGCR	<b>PLWDFSQFSR</b>	RSPRRRTPSPR	RSOSPRIR	RSOSPHARA	DIPOPHIN	RVTGGVEI VDK	SAGPCALR	SAICSVVR	SAICSVVRR	SALNPADDPSR	SCACIFICATION	STIPETTYVR	STLPETTWRR	STNPOSGR	STTDLEAYFK	HAELLAACHAH	אייו ופייו	TLPETTWARR	TLWKAGILYK	TLWKAGILYKR	TSAICSVVR	TSAICSVVRR	TTDLEAYFK	TSIGFCK COURSE	TWARAGA	TWARAGASPA	
	Position	45	738	775	Ξ	83	616 406	7 0 0 0 0	٥ (	8	86	86	20	710	179	169	189	106	128	376	183	167	167	000	357	65	520	520	771	262 64	170	170	85	104	716	- 12	171	150	150	519	519	105	278	176	176	
	Protein	ğ	ಕ್ಷ	걸	×	26	ಕ್ಷ ಜ	<u> </u>	전	헏	점 :	젍:	×	2 2	3 ≥	2	젙	젍	×	젙	3	2	2 :	3 2	3 €	ź×	젍	헏	점 8	ર્ચ >	ر د د	3	2	× ?	₹ \$	3 5	} } }	<u> </u>	ಕ್ಷ	젒		×	} } !	33	3	
	Frequency	19	2 8 5	9 -	16	15	8 4	0 6	20	15	17	17	90 f	- 0	. 4	5.	16	15	15	19	19	<u>۔</u> ای	5.	D C	- c	8 -	19	19	<b>8</b> ;		0 0	6.	16	<del>د</del> ز		D 0	<u> </u>	20	5 G	19	19	15	- T	9 9	16	
Table IX	Conservancy	95	90	06	80	75	0 0	0 6	001	7.5	82	82	06	0 0 0	000	75	80	75	7.5	95	95	7.5	75	n u	5 5	06	95	92	06	e 6	0 6 5	9 6	80	75	S 0	n 4	, c	100	100	95	95	75	s 6	0 80	80	

rable 1X				HBV A03 SUPER MOTIF (With binding information)	JPER	MOTIF (	With bindi	ng inforn	nation)				
Conservancy	Frequency	Protein	Position	Sequence	P2	C- term	АА	A*0301	A-1101	A-1101 A-3101	A-3301	A.6801	SEO ID NO:
96	18	×	133	MGGCRIFK		¥	8	0.0150	0.0002	-0.0005	-0.0009	0.0001	674
80	16	2	177	<b>NLOAGFFLLTR</b>	_	œ	Ξ						675
06	18	2	120	VSFGVWIR	တ	œ	æ	0.0040	0.0290	0.0750	0.0270	0.0360	929
100	20	젍	48	VSIPWTHK	တ	×	œ	0.0130	0.0170	0.0031	0.0013	0.0004	677
100	20	젙	358	VTGGVFLVDK	_	¥	10	0.0390	0.0920	0.0002	9000.0	0.0022	678
100	20	젙	378	WDFSQFSR	>	Œ	o	0.0015	0.0750	0.0013	0.0170	0.0330	616
80	16	N N	177	WRRAGRSPR	>	Œ	10	0.0027	0.0001				989
80	16	3	177	WARRGRSPAR	>	œ	Ξ						681
92	19	2	125	WIRTPPAYR	_	Œ	6	0.0008	0.0005				682
06	18	젍	314	MLOFFINSK	_	¥		-0.0002	0.0005	0.0020	0.0052	0.0001	683
82	17	2	56	WLWGMDIDPYK	_	×	1	0.0030	0.0013	-0.0003	0.0039	0.0490	684
100	20	<u>.</u> ਬ	122	YLPLDKGIK	_	¥	6	0.0001	0.0001	0.0006	9000.0	0.0002	685
06	18	3	118	YLVSFGVWIR	_	Œ	10	0.0005	0.0002				989
06	18	젍	538	YMDDVVLGAK	Σ	¥	10	0.0330	0.0043	0.0002	9000.0	0.0001	687
80	16	ర్జ	493	YSHPIILGFR	တ	œ	10						989
80	16	젗	493	YSHPIILGFRK	တ	×	=						989

	incy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID N
	95	19	POL	529	AFPHCLAF	XFXXXXXF		690
	95	19	POL	529	AFPHCLAFSY	XFXXXXXXXY		691
	95	19	POL	529	AFPHCLAFSYM	XFXXXXXXXXX		692
	95	19	×	62	AFSSAGPCAL	XFXXXXXXXL	0.0012	693
	90	18	POL	535	AFSYMDDVVL	XFXXXXXXXL	0.0009	694
	95	19	POL	655	AFTFSPTY	XFXXXXXY		695
	95	19	POL	655	AFTFSPTYKAF	XFXXXXXXXXXF		696 697
	95 90	19 18	POL	521	AICSVVRRAF AILCWGEL	XIXXXXXXXF		698
	90	18	NUC	58	AILCWGELM	XIXXXXXL		699
	95	19	NUC POL	58 642	ALMPLYACI	XIXXXXXXM XLXXXXXXI		700
	95	19	NUC	54	ALRQAILCW	XLXXXXXXXX		701
	80	16	BW	108	AMOWNSTTF	XMXXXXXXF		702
	95	19	POL	690	ATPTGWGL	XTXXXXXL		703
	75	15	POL.	690	ATPTGWGLAI	XTXXXXXXXI		704
	95	19	POL	397	AVPNLQSL	XVXXXXXL		705
	95	19	POL	397	AVPNLQSLTNL	XVXXXXXXXXL		706
1	100	20	NUC	131	AYRPPNAPI	XYXXXXXXI	0.0260	707
1	100	20	NUC	131	AYRPPNAPIL	XYXXXXXXXL	0.0220	708
	75	15	POL	607	CFRKLPVNRPI	XFXXXXXXXXXI		709
1	00	20	BW.	312	CIPIPSSW	XIXXXXXXW		710
1	00	20	BW.	312	CIPIPSSWAF	XIXXXXXXXF		711
	85	17	NUC	23	CLGWLWGM	XLXXXXXM		712
	85	17	NUC	23	CLGWLWGMDI	XLXXXXXXXI		713
	100	20	BW	253	CLIFLLVL	XLXXXXXL		714
	00	20	₽W ·	253	CLIFLLVLL	XLXXXXXXXL		715
	95	19	EW.	253	CLIFILVILDY	XLXXXXXXXXX		716
	95	19	EW.	239	CLRRFIIF	XLXXXXXF		717
	95	19	EW.	239	CLRRFIIFL	XLXXXXXXL		718
	75	15	EW.	239	CLRRFIIFLF	XLXXXXXXXF		719
	75	15	E//V	239	CLRRFIIFLFI	XLXXXXXXXXI		720
	100	20	EW	310	CTCIPIPSSW	XTXXXXXXXW	•	721
	90	18	NUC	3 1	DIDPYKEF	XIXXXXXF		722
	85	17	NUC	29	DLLDTASAL	XLXXXXXXL		723
	85	17	NUC	29	DLLDTASALY	XLXXXXXXXY		724
	95	19	POL	40	DENEGNENVSI	XLXXXXXXXXXI		725
	80	16	NUC	32	DTASALYREAL	XTXXXXXXXXL		726
	85	17	POL	618	DWKVCQRI	XWXXXXXI		727
	85 90	17 18	POL	618	DWKVÇQRIVGL DYQGMLPVCPL	XWXXXXXXXXL	0.0002	728 729
	80	16	₽W	262	BLGEEIRL	XYXXXXXXXXL	0.0002	729
	95	19	NUC X	122 43	ELLSFLPSDF	XLXXXXXL XLXXXXXXXF		731
•	95	19	NUC	43	ELLSFLPSDFF	XLXXXXXXXXXF		732
	90	18	NUC	117	EYLVSFGVW	XYXXXXXXW		733
	90	18	NUC	117	EYLVSFGVWI	XYXXXXXXXI	0.0340	734
	100	20	EW	382	FFCLWVYI	XFXXXXXI	0.00	735
	80	16	EW.	182	FFLLTRIL	XFXXXXXL		736
	80	16	BW.	182	FFLLTRILTI	XFXXXXXXXI		737
	85	17	BW.	13	FFPDHQLDPAF	XFXXXXXXXXXF		738
	80	16	BW	243	FIIFLFIL	XIXXXXXL		739
	80	16	EW/	243	FIIFLFILL	XIXXXXXXL		740
	80	16	EW.	243	FIIFLFILLL	XIXXXXXXXL		741
	80	16	· BW	248	FILLLCLI	XIXXXXXI	_	742
	80	16	BW.	248	FILLLCLIF	XIXXXXXXF		743
	80	16	₽W	248	FILLLCLIFL	XIXXXXXXXXL		744
	80	16	EW/	248	FILLLCLIFLL	XIXXXXXXXXL		745
	80	16	EW/	246	FLFILLLCL	XLXXXXXXL		746
	80	16	₽₩	246	FLFILLLCLI	XLXXXXXXXI		747
	80	16	BW/	246	FLFILLLCLIF	XLXXXXXXXF		748
	75	15	E/V	171	FLGPLLVL	XLXXXXXL		749
	95	19	POL	513	FLLAQFTSAI	XLXXXXXXXI		750
	95	19	POL.	562	FLLSLGIHL	XLXXXXXXL		751
	80	16	EW.	183	FLLTAILTI	XLXXXXXXI		752
	95	19	₽W	256	FLLVLLDY	XLXXXXXY		753
	95	19	BW/	256	FLLVLLDYQGM	XLXXXXXXXXM		754
	95	19	POL	656	FTFSPTYKAF	XTXXXXXXXXF		755
	95	19	POL	656	FTFSPTYKAFL	XTXXXXXXXXXL		756
	95	19	POL.	635	FTQCGYPAL	XTXXXXXXL		757
	95	19	POL .	635	FTQCGYPALM	XTXXXXXXXM		758
	95	19	₽W	346	FVGLSPTVW	XVXXXXXXW		759
	95	19	₽W	346	FVGLSPTVWL	XVXXXXXXL		760
	90	18	×	132	FVLGGCRHKL	XVXXXXXXL		761
	95	19	₽W	342	FVQWFVGL	XVXXXXXL		762
	90	18	POL	766	FVYVPSAL	XVXXXXXL		763
	95	19	POL	630	GFAAPFTQCGY	XFXXXXXXXXX		764
	80	16	₽W	181	GFFLLTRI	XFXXXXXI		765
	80	16	₽W	181	GFFLLTRIL	XFXXXXXXXL		766
	80	16	₽W	181	GFFLLTRILTI	XFXXXXXXXXXI		767
	95	19	₽W.	12	GFFPDHOL	XFXXXXXL		768
		4 5	EW	170	GFLGPLLVL	XFXXXXXXL		769
	75	15						
	75 80 95	16 19	POL POL	500 627	GFRKIPMGVGL GLLGFAAPF	XFXXXXXXXXXL XLXXXXXXXF		770 771

Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
100	20	BW	348	GLSPTVWL	XLXXXXXL		773
75	15	₽W	348	GLSPTVWLSVI	XLXXXXXXXI		774
85	17	NUC	29	GMDIDPYKEF	XMXXXXXXXF		775
90 90	18 18	EW POL	265 735	GMLPVCPL GTDNSVVL	XMXXXXXL		776
75	15	BW	735 13	GTNLSVPNPL	XTXXXXXL XTXXXXXXXL		777 778
80	16	POL	763	GTSFVYVPSAL	XTXXXXXXXXL		779
80	16	POL	507	GVGLSPFL	XVXXXXXL		780
80	16	POL	507	GVGLSPFLL	XVXXXXXL		781
95	19	NUC	123	GVWIRTPPAY	XVXXXXXXXY		782
· 85 85	17 17	NUC NUC	25 25	GWLWGMDI GWLWGMDIDPY	XWXXXXXXI		783 784
85	17	BW	65	GWSPQAQGI	XWXXXXXXXI	0.0024	785
. 85	17	EW.	65	GWSPQAQGIL	XWXXXXXXXL	0.0003	786
95	19	POL	639	GYPALMPL	XYXXXXXI,		787
95	19	POL.	639	GYPALMPLY	XYXXXXXXY	0.0490	788
95	19	₽W	234	GYRWMCLRRF	XYXXXXXXXF	0.0110	789
95 85	19 17	₽W	234	GYRWMCLRRFI GYSLNFMGY	XYXXXXXXXXI	0.0000	790
75	15	POL POL	579 579	GYSLNFMGYVI	XYXXXXXXXY XYXXXXXXXXXI	0.0002	791 792
80	16	POL.	820	HFASPLHVAW	XFXXXXXXXXW		793
75	15	POL	7	HFRKLLLL	XFXXXXXL		794
80	16	POL	435	HLLVGSSGL	XLXXXXXXL		795
75	15	POL	569	HUNPNKTKRW	XLXXXXXXXW		796
80	16	POL	491	HLYSHPII	XLXXXXXI		797
80 80	16 16	POL .	491	HLYSHPIIL	XLXXXXXXL		798
85	17 -	POL POL	491 715	HLYSHPIILGF HTAELLAACF	XLXXXXXXXXF XTXXXXXXXXF		799 800
100	20	NUC	52	HTALROAI	XTXXXXXI	·	801
95	19	NUC	52	HTALRQAIL	XTXXXXXXL		802
95	19	NUC	52	HTALRQAILCW	XTXXXXXXXXW		803
100	20	POL.	149	HTLWKAGI	XTXXXXXXI		804
100	20	POL	149	HTLWKAGIL	XTXXXXXXL		805
100 100	20 20	POL PO	149	HTLWKAGILY HYLHTLWKAGI	XTXXXXXXXY		806 807
100	20	POL BW	146 381	IFFCLWVY	XYXXXXXXXXI XFXXXXXY	•	808
100	20	E/V	381	IFFCLWVYI	XFXXXXXXI	0.0087	809
80	16	EW	245	IFLFILLL	XFXXXXXL		810
. 80	16	₽W	245	IFLFILLLCL	XFXXXXXXXL		811
80	16	BW.	245	IFLFILLLCLI	XFXXXXXXXXI		812
95 80	19	BW BW	255	IFLLVLLDY IIFLFILL	XFXXXXXXXY		813
80	16 16	EW EW	244 244	MFLFILLL	XIXXXXXL XIXXXXXXL		· 814 815
80	16	EW.	244	HFLFILLLCL	XIXXXXXXXXL		816
80	16	POL	497	IILGFRKI	XIXXXXXI		817
80	16	POL	497	IILGFRKIPM	XIXXXXXXXM		818
90	18	NUC	59	ILCWGELM	XLXXXXXM		819
80	16	POL	498	ILGFRKIPM	XLXXXXXXM		820
100 100	20 20	BW BW	249 249	ILLLCLIF ILLLCLIFL	XLXXXXXF XLXXXXXXL		821 822
100	20	BW	249	ILLLCLIFLL	XLXXXXXXXL		823
80	16	POL	760	ILRGTSFVY	XLXXXXXXY		824
95	19	₽₩	188	ILTIPOSL	XLXXXXXL	-	825
90	18	₽W	188	ILTIPOSLDSW	XLXXXXXXXXW	•	826
90	18	POL	625	IVGLLGFAAPF	XVXXXXXXXF	0.0004	827
85 95	17 19	EW	358	IWMMWYWGPS KFAVPNLQSL	XWXXXXXXXXL	0.0004 0.0020	828 829
80	16	POL POL	395 503	KIPMGVGL	XFXXXXXXXL XIXXXXXL	0.0020	830
80	16	POL	503	KIPMGVGLSPF	XIXXXXXXXXF		831
85	17	NUC	21	KLCLGWLW	XLXXXXXW		832
85	17	NUC	21	KLCLGWLWGM	XLXXXXXXXM		833
95	19	POL	489	KLHLYSHPI	XLXXXXXXI		834
80	16	POL.	489	KLHLYSHPII	XLXXXXXXXI		835
80 75	16 15	POL	489 108	KLHLYSHPIIL KLIMPARF	XLXXXXXXXXL		836 837
75 75	15	POL POL	108 108	KLIMPARFY	XLXXXXXF XLXXXXXXY		838
80	16	POL	610	KLPVNRPI	XLXXXXXI		839
80	16	POL	610	KLPVNRPIDW	XLXXXXXXXW		840
95	19	POL .	574	KTKRWGYSL	XTXXXXXXL		841
85	17	POL	574	KTKRWGYSLNF	XTXXXXXXXXF		842
85	17	POL	620	KVCORIVGL	XVXXXXXXL		843
85 95	17 19	POL	620	KVCQRIVGLL KVGNFTGL	XVXXXXXXXL		844 845
95 95	19 19	POL POL	55 55	KVGNFTGL	XVXXXXXL		845 846
85	17	X	91	KVLHKRTL	XVXXXXXXL		847
85	17	x	91	KVLHKRTLGL	XVXXXXXXXXL		848
100	20	POL	121	KYLPLDKGI	XYXXXXXXI	0.0028	849
	17	POL	745	KYTSFPWL	XYXXXXXL		850
85			745	KYTSFPWLL	XYXXXXXXL	3.6000	851
85	17	POL	745			5.0000	
85 80	16	ÐW.	247	LFILLLCL	XFXXXXXL	3.0000	852
85						-	

Conservancy	Freq	Protein	Position	Sequence	String	A:2401	SEQ ID NO:
100	20		254	LIFLLVLL	VIVVVVI		. 956
95	19	BW BW	254 254	LIFLLVILLDY	XIXXXXXXL		856 857
100	20	POL	109	LIMPARFY	XIXXXXXY		858
95	19	POL	514	LLAQFTSAI	XLXXXXXXI		859
100	20	₽W	251	LLCLIFLL	XLXXXXXL		860
100	20	BW BW	251	LLCUFLLVL	XLXXXXXXXL		861
100 85	20 17	NUC EW	251 30	LLCLIFLLVLL LLDTASAL	XLXXXXXXXXL XLXXXXXXL		862 863
85	17	NUC	30	LLDTASALY	XLXXXXXXXY		864
95	19	BW	260	LLDYQGML	XLXXXXXL		865
. 80	16	POL	752	LLGCAANW	XLXXXXXW		866
80	16	POL	752	LLGCAANWI	XLXXXXXXI		867
80 95	16 19	POL	752	LLGCAANWIL LLGFAAPF	XLXXXXXXXXL		868 869
. 75	15	POL BW	628 63	LLGWSPQAQGI	XLXXXXXF XLXXXXXXXXI		870
100	20	BW	250	LLLCLIFL	XLXXXXXXL		871
100	20	₽₩	250	LLLCUFUL	XLXXXXXXXL		872
100	20	₽W	250	LLLCLIFLLVL	XLXXXXXXXXXL		873
100	20	BW	378	LLPIFFCL	XLXXXXXL		874
100 100	20 20	₽W ₽W	378 378	LLPIFFCLW LLPIFFCLWVY	XLXXXXXXXXY		875 876
95	19	NUC	44	LLSFLPSDF	XLXXXXXXF		877
95	19	NUC	44	LLSFLPSDFF	XLXXXXXXXF		878
95	19	POL	563	LLSLGIHL	XLXXXXXXL		879
90	18	POL	407	LLSSNLSW	XLXXXXXW		880
90	18	POL ·	407	LLSSNLSWL	XLXXXXXXL		881
90 80	18 16	POL	407	LLSSNLSWLSL LLTRILTI	XLXXXXXXXXL		882 883
. 80	16	POL	184 436	LLVGSSGL	XLXXXXXI		884
95	19	BW	257	LLVLLDYQGM	XLXXXXXXXXM		885
95	19	₽W	257	LLVLLDYQGML	XLXXXXXXXXL		886
95	19	₽₩	175	LLVLQAGF	XLXXXXXF		887
95	19	Ew.	175	LLVLQAGFF	XLXXXXXXF		888
90 90	18 18	EW.	175	LLVLQAGFFL LLVLQAGFFLL	XLXXXXXXXL		889 890
100	20	EW EW	175 338	LLVPFVQW	XLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		891
100	20	BW	338	LLVPFVQWF	XLXXXXXXF		892
90	18	NUC	100	LLWFHISCL	XLXXXXXXL		893
85	17	NUC	100	LLWFHISCLTF	XLXXXXXXXXX		894
95	19	POL	643	LMPLYACI	XMXXXXXI		895
75 75	15 15	NUC NUC	137	LTFGRETVL LTFGRETVLEY	XTXXXXXXL		896 897
90	18	BW	137 189	LTIPOSLDSW	XTXXXXXXXXY		898
90	18	BW	189	LTIPQSLDSWW	XTXXXXXXXXW		899
90	18	POL	404	LTNLLSSNL	XTXXXXXXL		900
90	18	POL	404	LTNLLSSNLSW	XTXXXXXXXXXW		901
80	16	B₩	185	LTRILTIPOSL	XTXXXXXXXXXL		902
85 95	17 19	POL ENV	99 258	LTVNEKRRL LVLLDYQGM	XTXXXXXXL XVXXXXXXM		903 904
95	19	BW.	258	LVLLDYQGML	XVXXXXXXXL		905
95	19	BW.	176	LVLQAGFF	XVXXXXXF		906
90	18	EW.	176	LVLQAGFFL	XVXXXXXXL		907
90	18	B₩	176	LVLQAGFFLL	XVXXXXXXXL	•	908
100 95	20 19	BW.	339	LVPFVQWF LVPFVQWFVGL	XVXXXXXF	<i>:</i>	909
90	18	NUC BW	339 119	LVSFGVWI	XVXXXXXXXXL		910 911
100	20	POL	377	LVVDFSQF	XVXXXXXF		912
90	18	NUC	101	LWFHISCL	XWXXXXXL		913
85	17	NUC	101	LWFHISCLTF	XWXXXXXXXF		914
85	17	NUC	27	LWGMDIDPY	XWXXXXXXY		915
100 80	20	POL	151	LWKAGILY	XWXXXXXY		916
80	16 16	POL POL	492 492	LYSHPIIL LYSHPIILGF	XYXXXXXXL XYXXXXXXXXF	1.1000	917 918
85	17	BW.	360	MMWYWGPSL	XMXXXXXXL	0.0012	919
85	17	BW	360	MMWYWGPSLY	XMXXXXXXXY	0.0001	920
85	17	₽ <b>W</b>	361	MWYWGPSL	XWXXXXXL		921
85	. 17	BW	361	MWYWGPSLY	XWXXXXXXX	0.0027	922
. 95	19	POL.	561	NFLLSLGI	XFXXXXXI	2 2222	923
95 95	19 19	POL POL	561 42	NFLLSLGIHL NLGNLNVSI	XFXXXXXXXL XLXXXXXXXI	0.0099	924 925
95	19	POL	42	NLGNLNVSIPW	XLXXXXXXXXXX		926
90	18	POL	406	NLLSSNLSW	XLXXXXXXXW		927
90	18	POL	406	NLLSSNLSWL	XLXXXXXXXXL		928
95	19	POL	45	NLNVSIPW	XLXXXXXW		929
100	20	POL	400	NLQSLTNL	XLXXXXXL		930
100 75	20 15	POL	400	NLQSLTNLL NLSVPNPL	XLXXXXXXL		931
75 75	15	BW BW	15 15	NLSVPNPLGF	XLXXXXXXL XLXXXXXXXXF		932 933
80	16	POL	758	NWILRGTSF	XWXXXXXXXF		934
80	16	POL	758	NWILRGTSFVY	XWXXXXXXXXX		935
95	19	POL	512	PFLLAQFTSAI	XFXXXXXXXXI		936
95	19	POL	634	PFTQCGYPAL	XFXXXXXXXL	- 0.0002	937
95	19	POL	634	PFTQCGYPALM	XFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	<u>-</u> -	938

Conservancy	Freq	Protein	Position	Sequence	String	A:2401	SEQ ID NO:
	10	5.V	<del></del>	25/04/5/01	<del></del>		
95 85	19 17	POL.	341	PFVQWFVGL PIDWKVCQRI	XFXXXXXXL	0.0003	939 940
100	20	EW.	616 380	PIFFCLWVY	XIXXXXXXXI	•	941
100	20	BW	380	PIFFCLWVYI	XIXXXXXXXI		942
85	17	POL	713	PIHTAELL	XIXXXXXL		943
80	16	POL	496	PIILGFRKI	XIXXXXXXI		944
80	16	POL	496	PIILGFRKIPM	MXXXXXXXXIX		945
100	20	BW.	314	PIPSSWAF	XIXXXXXF		946
100	20	POL	124	. PLDKGIKPY	XLXXXXXXY		947
100	20	POL	124	PLDKGIKPYY	XLXXXXXXXY		948
95	19	POL	20	PLEEELPRL	XLXXXXXXXL		949
95	19 20	<b>₽</b> ₩	10	PLGFFPDHOL PLHPAAMPHL	XLXXXXXXXL		950 951
100 100	20	POL POL	427 427	PLHPAAMPHLL	XLXXXXXXXXL XLXXXXXXXXXL		952
100	20	EW	377	PLLPIFFCL	XLXXXXXXXL		953
100	20	BW	377	PLLPIFFCLW	XLXXXXXXXXW		954
95	19	EW.	174	PLLVLQAGF	XLXXXXXXF		955
95	19	₽₩	174	PLLVLQAGFF	XLXXXXXXXF		. 956
90	18	B₩	174	PLLVLQAGFFL	XLXXXXXXXXL		957
80	16	POL	711	PLPIHTAEL	XLXXXXXXL		958
80	16	POL	711	PLPIHTAELL	XLXXXXXXXL		959
75 75	15	POL	2	PLSYQHFRKL PLSYQHFRKLL	XLXXXXXXXL		960
75 85	15 1 <u>7</u>	POL POL	2 98	PLTVNEKRRL	XLXXXXXXXXL		961 962
80	16	POL.	505	PMGVGLSPF	XMXXXXXXXF		963
80	16	POL -	505	PMGVGLSPFL	XMXXXXXXXXL		964
80	16	POL	505	PMGVGLSPFLL	XMXXXXXXXXL		965
75	15	POL	692	PTGWGLAI	XTXXXXXI		966
85	17	POL.	797	PTTGRTSL	XTXXXXXL		967
85	17	POL	797	PTTGRTSLY	XTXXXXXXY		968
80	16	NUC	15	PTVQASKL	XTXXXXXL	•	969
80	16	NUC	15	PTVQASKLCL	XTXXXXXXXL		970
75 75	15 15	BW BW	351	PTVWLSVI PTVWLSVIW	XTXXXXXI		971
75 75	15	BW BW	351 351	PTVWLSVIWM	XTXXXXXXW XTXXXXXXXM		972 973
85	17	POL	612	PVNRPIDW	XVXXXXXW		974
80	16	POL	750	PWLLGCAANW	xwxxxxxxxx		975
80	16	POL.	750	PWLLGCAANWI	XWXXXXXXXI		976
100	20	POL	51	PWTHKVGNF	XWXXXXXXF	0.0290	977
80	16	×	8	QLDPARDVL	XLXXXXXXL		978
80	16	×	8	QLDPARDVLCL	XLXXXXXXXXL		979
90	18	NUC	99	QLLWFHISCL	XLXXXXXXXL		980
95	19	POL	685	QVFADATPTGW QWFVGLSPTVW	XVXXXXXXXXX		981
95 75	19 15	BW 8W	344 242	RFIIFLFI	XWXXXXXXXX		982 983
75 75	15	. BW	242	RFIIFLFIL	XFXXXXXXXL		984
75	15	₽W	242	RFIIFLFILL	XFXXXXXXXXL		985
75	15	EW.	242	RFIIFLFILLL	XFXXXXXXXXXL		986
100	20	₽₩	332	RFSWLSLL	XFXXXXXL		987
100	20	₽W	332	RFSWLSLLVPF	XFXXXXXXXXF		988
80	16	₽W	187	RILTIPOSL	XIXXXXXXL		989
90	18	POL	624	RIVGLLGF	XIXXXXXF		990
75	15	POL	106	RLKLIMPARF	XLXXXXXXXF	•	991
75 05	15 19	POL.	106	RLKLIMPARFY RLVVDFSQF	XLXXXXXXXXY	•	992 993
95 90	18	POL POL	376 353	RTPARVTGGVF	XLXXXXXXF XTXXXXXXXXF		994
95	19	POL	36	RVAEDLNL	XVXXXXXL		995
90	18	POL.	36	RVAEDLNLGNL	XVXXXXXXXXX		996
80	16	POL	818	RVHFASPL	XVXXXXXL		997
100	20	POL	357	RVTGGVFL	XVXXXXXL		998
85	17	POL	577	RWGYSLNF	XWXXXXXF		999
85	17	POL	577	RWGYSLNFM	MXXXXXXXX		1000
85	17	POL	577	RWGYSLNFMGY	XWXXXXXXXY		1001
95	19	BW.	236	RWMCLRRF	XWXXXXXF		1002
95 95	19	BW.	236	RWMCLRRFI	XWXXXXXXI	0.0710	1003
95	19 19	EW BW	236 236	RWMCLRRFII RWMCLRRFIIF	XWXXXXXXXI	1.1000	1004 1005
100	20	POL	167	SFCGSPYSW	XFXXXXXXXW	0.0710	1006
95	19	NUC	46	SFLPSDFF	XFXXXXXXF	3.3710	1007
80	16	POL	765	SFVYVPSAL	XFXXXXXXL		1008
100	20	POL	49	SIPWTHKVGNF	XIXXXXXXXXF		1009
95	19	BW	194	SLDSWWTSL	XLXXXXXXXL		1010
95	19	₽W	194	SLDSWWTSLNF	XLXXXXXXXXF		1011
95	19	POL	416	SLDVSAAF	XLXXXXXF		1012
95	19	POL	416	SLDVSAAFY	XLXXXXXXY		1013
100	20	₽W	337	SLLVPFVQW	XLXXXXXXXW		1014
100	20	BW	337	SLLVPFVQWF	XLXXXXXXF		1015
75	15	POL.	581	SUNFMGYVI	XLXXXXXXI		1016
95	19	X	54	SLRGLPVCAF	XLXXXXXXXF		1017
90 75	18 15	POL	403 104	SLTNLLSSNL STTDLEAY	XLXXXXXXXL		1018 1019
75 75	15	X X	104	STIDLEAT	XTXXXXXY XTXXXXXXF		1019
. 75	15	₽w.	17	SVPNPLGF	XVXXXXXF	<del></del>	1021
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Conservancy	Freq	Protein	Position	Sequence	String	A*2401	SEQ ID NO:
85	17	POL	548	SVQHLESL	XVXXXXXL		1022
80	16	BW	330	SVRFSWLSL	XVXXXXXXL	•	1023
80	16	BW.	330	SVRFSWLSLL	XVXXXXXXXL		1024
90 85	18 17	POL.	739 730	SVVLSRKY SVVLSRKYTSF	XVXXXXXY		1025
95	19	POL POL	739 524	SVVRRAFPHCL	XVXXXXXXXF XVXXXXXXXXL		1026 1027
95	19	POL	413	SWLSLDVSAAF	XWXXXXXXXXXF		1028
100	20	EW.	334	SWLSLLVPF	XWXXXXXXF	0.3900	1029
95	19	POL	392	SWPKFAVPNL	XWXXXXXXXL	5.6000	1030
100	20	BW.	197	SWWTSLNF	XWXXXXXF		1031
· 95 90	19	BW	197	SWWTSLNFL	XWXXXXXXXL	0.3800	1032
75	18 15	POL POL	537 4	SYMDDVVL SYQHFRKL	XYXXXXXL		1033 1034
. 75	15	POL	4	SYQHFRKLL	XYXXXXXXXL	0.0051	1035
75	15	POL	4	SYQHFRKLLL	XYXXXXXXXL	0.0660	1036
75	15	POL	4	SYQHFRKLLLL	XYXXXXXXXXL		1037
75	15	NUC	138	TFGRETVL	XFXXXXXL		1038
75 75	15	NUC	138	TEGRETYLEY	XFXXXXXXXXY		1039
75 95	15 19	NUC POL	138 657	TFGRETVLEYL TFSPTYKAF	XFXXXXXXXXXL XFXXXXXXXF	0.0060	1040 1041
95	19	POL	657	TFSPTYKAFL	XFXXXXXXXXL	0.0043	1042
90	18	EW	190	TIPQSLDSW	XIXXXXXXW		1043
90	18	EW.	190	TIPOSLDSWW	XIXXXXXXXIX		1044
100	20	POL	150	TLWKAGIL	XLXXXXXL		1045
100 75	20	POL	150	TLWKAGILY	XLXXXXXXY		1046
75 85	15 17	POL.	105 798	TTDLEAYF TTGRTSLY	XTXXXXXF XTXXXXXY		1047 1048
85	17 -	POL	100	TVNEKRRL	XVXXXXXL		1049
80	16	NUC	16	TVQASKLCL	XVXXXXXXL		1050
80	16	NUC	16	TVQASKLCLGW	XVXXXXXXXXX		1051
75	15	BW	352	TVWLSVIW	XVXXXXXW		1052
75 05	15	EW SS	352	TVWLSVIWM	XVXXXXXXM	0.0100	1053
95 75	19 15	POL X	686 131	VFADATPTGW VFVLGGCRHKL	XFXXXXXXXXXW XFXXXXXXXXXXL	0.0180	1054 1055
85	17	ροL	543	VLGAKSVQHL	XLXXXXXXXL		1056
90	18	×	133	VLGGCRHKL	XLXXXXXXL		1057
85	17	×	92	VLHKRTLGL	XLXXXXXXL		1058
95	19	BW	259	VLLDYQGM	XLXXXXXM		1059
95 95	19 19	: EW	259	VLLDYQGML VLQAGFFL	XLXXXXXXXL		1060
95	19	EW EW	177 177	VLQAGFFLL	XLXXXXXXL XLXXXXXXXL		1061 1062
85	17	POL	741	VLSRKYTSF	XLXXXXXXF		1063
85	17	POL	741	VLSRKYTSFPW	XLXXXXXXXXXX		1064
80	16	POL	542	VVLGAKSVQHL	XVXXXXXXXXL		1065
85	17	POL	740	VVLSRKYTSF	XVXXXXXXXF		1066
95 95	19 19	POL NUC	525 124	VVRRAFPHCL VWIRTPPAY	XVXXXXXXXXL		1067 1068
75	15	BW	353	VWLSVIWM	XWXXXXXM		1069
90	18	NUC	102	WFHISCLTF	XFXXXXXXXF	0.0300	1070
95	19	₽₩	345	WFVGLSPTVW	XFXXXXXXXX	0.0120	1071
9.5	19	₽W	345	WFVGLSPTVWL	XFXXXXXXXXL		1072
80	16	, POL	759 760	WILRGTSF WILRGTSFVY	XIXXXXXF		1073
80 95	16 19	POL NUC	759 125	WIRTPPAY	XIXXXXXXY	• .	1074 1075
80	16	POL	751	WLLGCAANW	XLXXXXXXW		1075
80	16	POL.	751	WLLGCAANWI	XLXXXXXXXI		1077
80	16	POL.	751	WLLGCAANWIL	XLXXXXXXXXL		1078
95	19	POL.	414	WLSLDVSAAF	XLXXXXXXXF		1079
95 100	19 20	POL.	414	WLSLDVSAAFY WLSLLVPF	XLXXXXXXXXX		1080
100	20	BW BW	335 335	WLSLLVPFVQW	XLXXXXXF XLXXXXXXXXXW		1081 1082
85	17	NUC	26	WLWGMDIDPY	XLXXXXXXXX		1083
95	19	BW.	237	WMCLRRFI	XMXXXXXI		1084
95	19	₽W	237	WMCLRRFII	XMXXXXXXI	0.0230	1085
95	19	BW	237	WMCLRRFIIF	XMXXXXXXXF	0.0013	1086
95 85	19 17	BW BW	237	WMCLRRFIIFL WMMWYWGPSL	XMXXXXXXXL XMXXXXXXXL	0.0005	1087 1088
85 85	17	BW .	359 359	WMMWYWGPSL	XMXXXXXXXXXX	0.0005	1088
100	20	POL	52	WTHKVGNF	XTXXXXXF		1099
95	19	POL	52	WTHKVGNFTGL	XTXXXXXXXXL		1091
95	19	₽W	198	WWTSLNFL	XWXXXXXL		1092
85	17	₽W	362	WYWGPSLY	XYXXXXXY	0.0001	1093
100	20	POL	147	YLHTLWKAGI YLHTLWKAGIL	XLXXXXXXXI		1094
100 100	20 20	POL POL	147 122	YLPLDKGI	XLXXXXXXXXL XLXXXXXXI		1095 1096
100	20	POL POL	122	YLPLDKGIKPY	XLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		1097
90	18	NUC	118	YLVSFGVW	XLXXXXXXW		1098
90	18	NUC	118	YLVSFGVWI	XLXXXXXXI		1099
85	17	POL.	746	YTSFPWLL	XTXXXXXL		1100

HBV B07 SUPER MOTIF (With binding information)

SEQIDNO	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1124	1123	9711	1127	0711	1129	130	2	132	1133	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148
B-5401		0.0002	1.4000	0.0093						0.0001	0.0019			0.0021	0.0199	0.0480				0.0035	0.0002	0.0001	0.0065	0.0002	9000	0.000	0.000	0.0100	0.0170		0.060.0	0.0030	0.4500						0.0002	0.0035		0.0002	0.0021		0.0005	0.3300	2.7500	
B*5301		0.0002	0.0002	-0.0003						0.0001	0.0002			0.0011	0.5400	0.0790				0.0002	0.0001	-0.0003	0.0002	0000	0000	0000	0.000	0.0037	0.0300	0.0	0000	0.0002	0.7430						0.0001	0.1400		9000.0	0.0139		0.3100	0.0016	0.0120	
B*5101		0.0019		0.0004						0.0001	0.0019			0.0003	0.0665	0.0900				0.0001	0.0002	0.0001	0.0110	2000	0.000	0.00	0.00	0.3	0.00	0.00.0	0	0.0019	2000						0.0007	0.0360		0.0002	0.0043		0.0052		-0.0003	
B*3501	-	0.0012	0.0001	0.0010						0.0001	0.0001			0.0016	0.5250	0.2200				0.0001	0.0001	0.0001	0.0001	0000	2000	0000	0.000	0.0004	0.000	0.000	4000	9.767.9	0.0024						0.0001	0.0001		0.0079	0.0001		0.0630	0.0011	0.0027	
B.0702		0.0001	0.0029	0.2300			-			0.0120	0.0001			0.0002	0.0001	0.0990				0.0900	0.0001	-0.0002	0.0003	0000	0.000	0.00	20.0	0.000.0	0.0360	9.0	7000	0.004	0.130	2					0.0013	0.0001		0.0002	0.0002		0.0040	0.0018	0.0000	
AA	6	8	10		6	o.	11	o	æ	თ	80	-	o	10	6	10	80	თ	11	10	10	-	œ	, t		- •	_ c	<b>o</b> c	,	2	) a	<b>o</b> a	, <del>-</del>	) C		΄ <b>ω</b>	6	80	10	80	6	10	. 11	89	6	10		10
C. term	∢	>	∢	_	_	_	_	_	>	_	¥	>	∢	u.	>	≥	⋖	⋖		∢	_	<	: ∢	. u	. u		. ر	_ د	< د	• -	- <	ÇЦ	- ∢	C LL		>	≥	4	u_	≥	>	>	_	_	_	∢	∢	ر
P2	۵	۵.	۵.	۵	۵	۵	م	۵	۵.	٩	۵.	٩	۵	۵.	٩	۵	۵	۵	٩	۵.	۵.	۵	۵.	. 0.	۵ ـ	۵ م		. 0	_ 0	_ 0	. 0	۵ ـ	۵ ـ	۵.	. a	۵	٩		<u> </u>	۵	۵.	<b>م</b>	م	۵.	۵.	<u>a</u>	<u>a</u>	<b>_</b> -∙
Sequence	APCNFFTSA	APFTQCGY	APFTQCGYPA	APFTQCGYPAL.	CPGYRWMCL	CPIVQASKL	CPTVQASKLCL	DPARDVLCL	DPRVRGLY	DPSRGPLGL	DPYKEFGA	<b>FPAGGSSSGTV</b>	FPDHQLDPA	FPDHOLDPAF	FPHCLAFSY	<b>FPHCLAFSYM</b>	<b>FPWLLGCA</b>	<b>FPWLLGCAA</b>	<b>FPWLGCAANW</b>	GPCALRFTSA	GPLEEDPR	GPLEEELPRLA	GPLLVLOA	GPLLVLOAGE	GPI VI OAGEF	GPI TANEKBBI	חסאאיסח	HPAAMPHII	HPAAMPHI I V	HPIII GFRKI	AWSSAIGI	IPIPSSWAF	IPIPSSWAFA	IPMGVGLSPF	IPMGVGLSPFL	<b>IPOSLDSW</b>	<b>IPOSLDSWW</b>	IPSSWAFA	<b>PWTHKVGNF</b>	LPIFFCLW	LPIFFCLWV	LPIFFCLWVY	LPIFFCLWYI	LPIHTAEL	LPIHTAELL	LPIHTAELLA	LPIHTAELLAA	LPKVLHKRTL
Position	146	633	633	633	232	4	4	10	122	778	33	130	4	14	530	530	749	749	749	29	19	19	173	173	173	2.0	7.7	429	429	495	3 6	. E.	313	504	504	191	191	315	50	379	379	379	379	712	712	712	712	<del>ර</del> ි ස
Protein	×	점	젙		<b>}</b>	3	3	×	<b>%</b>	점	3	8	&	<u>₹</u>	ಶ	절	젍	ಕ	젙	×	전	젙	<b>8</b>	26	<u></u>	5 6	3 5	₫ ⊊	2	2	<u>}</u>	<u></u>	<u></u>	<u> </u>	젍	2	<b>8</b>	2		<b>≥</b>	8	2	2	ಕ	헏	ಕ್ಷ	ğ	×
Frequency	15	19	19	19	20	16	16	16	16	18	18	15	18	17	19	19	15	15	15	18	19	18	19	19	0 0			0 0	17	. 4	0.0	200	16	16	16	18	18	16	20	20	20	20	20	17	17	17	17	16
Conservancy Frequency Protein		95	92	92	100	0 8	80	80	80	06	06	7.5	06	85	92	92	7.5	7.5	7.5	06	92	06	. 6	- 6	. v	י ער מי	3 5	8 5	8.5	0 6	9 6	001	80	80	80	90	90	80	100	100	100	100	100	82		82	82	80

HBV B07 SUPER MOTIF (With binding information)

. Table XI

123 LPLDKGIKPYY 58 LPVCAFSSA 611 LPVNRPIDWW 611 LPVNRPIDWW 433 MPH.LLVGSSGL 1 MPLSYOHFRU 774 NPADDPSRGRL 9 NPLGFPDVAL 571 NPWCTRRWGY 129 PPAYRPPNA 129 PPAYRPPNA 129 PPAYRPPNA 129 PPAYRPPNA 129 PPAYRPPNA 134 PPNAPILSTL 615 RPIDWKVCORI 133 RPPNAPILSTL 615 SPHLAOFTSA 14 SPEHCSPHTA 511 SPFLLAOFTSA 49 SPHHTALROA 67 SPOAGOIL 67 SPHTALROA 67 SPHTALROA 67 SPHTALROA 67 SPHTALROA 67 SPOAGOIL	IKPY SSA SSA P SSA P SSGL DW SSGL P SSGL P SFF F F F F F F F F F F F F F F F F F	>> < >> > + > + < > > + + + + + + + + +	5	0.0001 0.0480 0.0480 0.0480 0.00120 0.0012 0.0001 0.0001 0.0001 0.0001 0.0001 0.0002 0.0002 0.0002 0.0002	0.0290 0.0009 0.0710 0.0097 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001	0.0002 0.0001 0.0110 0.0110 0.0001 0.0001 0.0035 0.0036 0.0018 0.0001	0.0003 0.0009 0.0009 0.0370 0.0028 0.0003 0.0003 0.0003 0.0003 0.0003 0.0003	0.0002 0.0001 19.0000 0.0190 0.0001 0.0002 0.0002 0.0002 0.0001	1149 1151 1152 1153 1154 1155 1156 1160 1160 1160 1160 1160 1160
	•	> < \$ > \$ - > < 4 - \$ 4 # 4 4		0.0002 0.0480 0.0480 0.0012 0.0012 0.0001 0.0001 0.0007 0.0007 0.0002 0.0002 0.5500 0.0820	0.0009 0.0710 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001	0.0001 0.0110 0.0110 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001	0.0009 0.0009 0.0003 0.0003 0.0003 0.0003 0.0003 0.0003 0.0003	0.0001 0.0001 0.0001 0.0001 0.0002 0.0002 0.0002	1150 1152 1152 1153 1154 1156 1160 1160 1160 1160 1160 1160 1160
	•	√ > > - + + + + + + + + + + + + + + + + +	6 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0.0480 0.00011 0.00120 0.00011 0.0001 0.0001 0.00076 0.1300 0.0002 0.5500 0.0820	0.0010 0.0097 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001	0.0110 0.0120 0.0001 0.0001 0.0001 0.0035 0.0038 0.0001 0.0001	0.0009 0.0370 0.0028 0.0003 0.0003 0.0003 0.0003 0.0003 0.0003	0.0000 0.0001 0.0001 0.0002 0.0002 0.0002 0.0001	1151 1152 1153 1154 1156 1160 1160 1160 1160 1160 1160 1160
	•	>> > - >	9	0.0001 · 0.0001 · 0.0001 · 0.0001 · 0.0001 · 0.0001 · 0.0001 · 0.0001 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002 · 0.0002	0.0094 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0.0120 0.0001 0.0001 0.0001 0.0001 0.0035 0.0036 0.0001 0.0001	0.0370 0.0003 0.0002 0.0003 0.0003 0.0003 0.0003 0.0003	0.0190 0.0001 0.0001 0.0002 0.0002 0.0002 0.0001	1152 1153 1154 1156 1159 1160 1160 1160 1160 1160 1160 1160 116
		>		0.0001 . 0.00120 0.0012 0.0001 0.0001 0.0001 0.0007 0.1300 0.5500 0.0820	0.0099 0.00099 0.00099 0.00099 0.00099	0.0120 0.0001 0.0001 0.0001 0.0001 0.0035 0.0036 0.0001 0.0001	0.0370 0.0003 0.0028 0.0003 0.0003 0.0003 0.0003 0.0003 0.0003	0.0190 0.0001 0.0001 0.0002 0.0002 0.0002 0.0001	1153 1156 1156 1158 1159 1169 1169 1169 1169 1169
			-	0.0001. 0.00120 0.0012 0.0001 0.0001 0.0001 0.0076 0.1300 0.5500 0.0820	0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.00	0.0120 0.0001 0.0001 0.0001 0.0035 0.0280 0.0018 0.0001	0.0370 0.0003 0.0028 0.0003 0.0003 0.0003 0.0003 0.0003 0.0003	0.0190 0.0001 0.0001 0.0002 0.0002 0.0002 0.0001	1156 1156 1158 1158 1169 1169 1168 1168 1168 1168 1168
		≥ - > + 4 + 4 + 4 + 4 + 4 + 4 + 4 + 4	•	0.00120 0.00120 0.0001 0.0001 0.00076 0.1300 0.5500 0.0820	0.00.00 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000	0.0003 0.0003 0.0003 0.0003 0.0003 0.0003 0.0003	0.0001 0.0001 0.0002 0.0002 0.0002 0.0002	155 155 155 165 166 167 168 168 168 168 168 168 168 168 168 168
		• • • • • • • • • • • • • • • • • • •	:	0.0120 0.0012 0.0001 0.0001 0.0007 0.0007 0.1300 0.5500 0.0820	0.000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0.0001 0.0001 0.0001 0.0035 0.0038 0.0018	0.0003 0.0003 0.0003 0.0003 0.0003 0.0003 0.0003 0.0003	0.0001 0.0003 0.0002 0.0002 0.0002 0.0002	1169 1160 1160 1160 1160 1160 1160 1160
		• • • • • • • • • • • • • • • • • • •	: T & 2 & T & C T & T T	0.0001 0.0001 0.0001 0.00076 0.1300 0.5500	0.000 0.000	0.0001 0.0001 0.0035 0.0038 0.0018 0.0001	0.0028 0.0003 0.0003 0.0001 0.0002 0.0003 0.0003	0.0001 0.0003 0.0002 0.0002 0.0002 0.0001	1160 1160 1160 1160 1160 1160 1160 1160
		>> 4 - > + 4 # 4 4	8 <sup>2</sup> • <sup>2</sup> • <sup>2</sup> • <sup>2</sup> • <sup>2</sup> • <sup>2</sup> • <sup>2</sup>	0.0001 0.0003 0.0001 0.0007 0.0007 0.1300 0.5500 0.0820	0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000	0.0001 0.0001 0.0035 0.0038 0.0018 0.0001	0.0002 0.0003 0.0003 0.0001 0.0002 0.0003 0.0003	0.0003 0.0001 0.0002 0.0002 0.0001	1159 1160 1161 1162 1163 1164 1166 1166 1169
		> 4 - 3 4 # 4 4	2 o	0.0001 0.0001 0.0001 0.0007 0.0007 0.1300 0.5500 0.0820	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0.0001 0.0001 0.0035 0.0038 0.00018 0.0001	0.0003 0.0003 0.0003 0.0001 0.0002 0.0003	0.0003 0.0001 0.0002 0.0002 0.0001	1160 1162 1163 1164 1165 1166 1167
		4 - ≥ × 4 + 4 •	ο <u>Γ</u> ο <u>Ο Γ</u> α <u>Γ</u> Γ	0.0001 0.0003 0.0001 0.0001 0.0076 0.1300 0.5500 0.0820	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0.0001 0.0001 0.0035 0.0038 0.00018 0.0001	0.0003 0.0003 0.0001 0.0001 0.0003 0.0003	0.0003 0.0001 0.0002 0.0002 0.0001	1162 1163 1164 1165 1166 1169 1169
		- ≥ × × × ×	_ 0 0 <u>_</u> ∞ <u>_</u>	0.0003 0.0001 0.0001 0.0076 0.1300 -0.0002 0.5500 0.0820	0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000	0.0001 0.0001 0.0035 0.00018 0.0001 0.0001	0.0003 0.0001 0.0001 0.0002 -0.0003	0.0001 0.0002 0.0002 0.0001	1162 1163 1164 1165 1166 1169 1169
		> × × × × × × × × × × × × × × ×	o 0	0.0001 0.0001 0.0076 0.1300 -0.0002 0.5500 0.0820	0.0002 0.0001 0.0001 0.0001 0.0001	0.0001 0.0035 0.00280 0.00018 0.0001	0.0003 0.0003 0.0003 0.0003	0.0002 0.0002 0.0001	1163 1164 1165 1166 1167 1169 1169
		→ → → → ← ← ◆	0 1 8 1 1	0.0001 0.0076 0.1300 -0.0002 0.5500 0.0820	00000000000000000000000000000000000000	0.0035 0.0280 0.0018 0.0018 0.0180	0.0001 0.0002 -0.0003 0.0003	0.0002 0.0002 0.0001	1165 1165 1167 1168 1169
			= <del>-</del>	0.0076 0.1300 -0.0002 0.5500 0.0820	0.0001 0.0001 0.0001 0.0009 0.0001	0.0280 0.0018 0.0001 0.0180	0.0002 -0.0003 -0.0003	0.0002 0.0001 0.0011	1165 1166 1167 1169
			∞ <del>I</del> I	0.0076 0.1300 -0.0002 0.5500 0.0820	0.0001 0.0001 0.0009 0.0009 0.0001	0.0280 0.0018 0.0001 0.0180 0.0001	0.0002 -0.0003 -0.0003	0.0002 0.0001 0.0011	1166 1167 1169 1169
		J ≪ F ≪ ≪	==	0.1300 -0.0002 0.5500 0.0820	0.0001 0.0001 0.0009 0.0001	0.0018 0.0001 0.0180 0.0001	-0.0003 -0.0003 0.0009	0.0001	1168 1168 1169 1170
		<b>∢</b> ¼ ∢ ∢	=	-0.0002 0.5500 0.0820	0.0001 0.0009 0.0001 0.0001	0.0001 0.0180 0.0001	0.0003	0.0011	1168 1169 1170
		<b></b> ∢ ∢		0.5500 0.0820	0.0009 0.0001 0.0001	0.0180	. 6000°u	****	1169
		∢ ∢	80	0.0820	0.0001	0.0001	,	0.0093	1170
		٧	11		0.0001		-0.0003	12.0500	1
		c	10	0.0012			0.0002	0.0035	1171
		_	=	0.5800	0.0001	0.0004	0.0005	0.0002	1172
		ر	80						1173
		_	8						1174
		>	80						1175
		_	o						1176
		3	10						1177
S.		Σ	=				,		1178
		ب	80	0.3900	0.0001	0.0019	0.0002	0.0002	1179
		>	<b>o</b>	0.0078	0.0001	0.0013	0.0001	0.0015	1180
,		u.	10	0.3200	0.1000	0.0001	0.0099	0.0006	1181
			= :	0.0950	0.0001	0.0001	0.0005	0.0005	1182
_		∢ .	2	0.0001	0.000.0		0.0002	0.0	1183
57 IPPROBLE	15% 15%	3 ب	æ <b>Ş</b>						1384
		Α.	2 '						183
,	-	⋖	œ						1186
•		_	6					,	1187
		>	æ	0.0010	0.0001	19.0000	0.0002	0.1100	1188
_	₽VGL P		10	0.0011	0.0001	0.0100	0.0001	0.0025	1189
		_	10	9000.0	0.0001	0.0004	0.0001	0.0002	1190
>	LTNLL P	ب	=	0.0004	0.0001	0.0001	-0.0003	0.0002	1191
769 VPSALNPA		4	æ	0.0011	0.0001	0.0070	0.0002	1.0000	1192
393 WPKFAVPNL	VPNL P	_	6	0.0054	0.0002	0.0015	0.0001	0.0015	1193
640 YPALMPLY		>-	80	0.0004	0.2600	0.4100	0.0450	0.0056	1194
640 YPALMPLYA	PLYA P	۷	<b>о</b>	0.0180	0.0480	0.0340	0.0140	16.0000	1195
640 YPALMPLYACI	-	_	Ξ	0.0040	0.0001	0.0470	0.0320	0.0700	1196

TABLE XII		HBV B27 Super Mot	HBV B27 Super Motif (No binding data available)	<u>lable)</u>	·	
Protein	Sequence	Position in HBV	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SeqID Num
						1197
AYW	AHLSLRGL	51	8	19	95	1198
AYW	ARVTGGVF	356	89	18	06	1199
AYW	DHGAHLSL	48	<b>©</b>	19	95	1200
AYW	DHOLDPAF	16	œ (	8	06	1201
AYW	DKGIKPYY	126	<b>6</b> 0 (	20	100	1202
AYW	FHISOLIF	103	<b>&amp;</b>	18	06	1203
AYW	FRKIPMGV	501	œ (	. 16	80	1204
AYR	CHEIVLEY	140	<b>∞</b> (	15	75	1205
AYW	HHIALKUA	16	<b>∞</b> α	50	100	1206
AYW	INTAELLA	4-7	το (	17	32	1207
AYW	LHKHILGL			- 18	06	1208
AYW	LALYSHPI	490	<b>6</b> 0 (	19	95	1209
AYW	LRGLPVCA	ို့	<b>∞</b>	19	95	1210
ΑΥW	LRGTSFVY	761	<b>6</b> 0	16	80	1211
AYW	LROAILCW	55	89	19	98	1212
AYW	LARFIIFL	240	89	19	95	1213
AYW	NKTKRWGY	573	ಹ	15	7.5	1214
AYW	NRPIDWKV	614	8	18	06	1215
AYW	NRRVAEDL	34	<b>&amp;</b>	17	85	1216
AYW	PHCLAFSY	531	œ	6 !	95	1217
AYW	PHGGLLGW	200	<b>x</b> 0 (	17	82	1218
AYW	A TAVPINE	400		B .		6121
		0 7	σα	د د و	د / د /	1220
****	BKYTSEPW	777	ο α	20	100 8£	1221
AVA AVA	BBAFPHC	707	ာဏ		0 0	1223
****	BREITH	26.7	ာဏ	. T	9 4	1224
**************************************	35 III.dHS	494	ο	2 4	· 0	1225
W.A	SKICIGW	20	) <b>c</b> c	5 6	9 5	1226
W.A	SBNLYVSI	472	) (()	5 4	2 6	1227
AYW	TKRWGYSL	575	- α	9 -		1228
AYW	TRHYLHIL	144	æ	50	100	1229
AYW	VRFSWLSL	331	89	16	80	1230
AYW	WKVCQRIV	619	89	17	85	1231
AYW	YRPPNAPI	132	80	20	100	1232
AYW	ARVTGGVFL	356	6	. 81	06	1233
AYW	EHCSPHIHTA	46	თ	50	100	1234
AYR	GRETMEN	140	O	15	7.5	1235
AYW	HHTALROAI	. 51	6	20	100	1236
AYW	HKVGNFTGL	54	တ	19	95	1237
AYW	IHTAELLAA	714	თ	17	85	1238
AYW	KRWGYSLNF	576	<b>o</b>	17	85	1239
AYW	LHLYSHPII	490	<b>o</b>	16	80	1240
AYW	LHPAAMPHL	428	<b>o</b>	20	100	1241
AYW	LHTLWKAGI	148	ത	20	100	1242

HBV B27 Super Motif (No binding data available)

, TABLE XII

		HBV	Amino Acids	Frequency	(%)	
AYR	LKLIMPARF	107	6	1.5	7.5	1243
M.A	LRGLPVCAF	: v:	, o	9	. o	1244
AYW	LAGTSFVVV	761	ത	. 4	S &	1245
ΑΥW	IBBEIELF	240	σ	, <del>L</del>	) (A	1246
AYW	PHCLAFSYM	531	, o	2 5	. o	1247
ΑΥW	PHHTALBOA	50	· თ	0.00	201	1248
ΑΛW	PKVI HKBTI	0 6	, o		\$ c	1249
AVB.	- III JAHAN	; cc	, <b>o</b>	- <del>-</del>	, v	1250
W.V.V	CHICALIGE	, co	, o	•		1251
N/A	BKIPMGVGI	502	ກອ	٠ ټ	) (	1252
A A		200		0 (	0.6	707
Arw	מיטבטנטויט	500	<b>.</b> .	9 !	08	507
AYW	HAYISHWL	/44	י מ	17	82	1254
ΑΥW	RRAFPHCLA	527	6	19	95	1255
AYW	RRFIIFLFI	241	6	15	7.5	1256
AYR	RRLKLIMPA	105	6	15	7.5	1257
AYW	RRVAEDLNL	35	6	18	06	1258
AYW	SKLCLGWLW	20	6	17	85	1259
AYW	SRKYTSFPW	743	6	17	85	1260
AYW	TRHYLHILW	144	6	20	100	1261
AYW	VHFASPLHV	819	6	16	80	1262
AYW	VRFSWLSLL	331	6	16	80	1263
AYW	VRRAFPHCL	526	6	19	9.6	1264
AYW	YRPPNAPIL	132	თ	20	100	1265
AYW	YRWMCLARF	235	თ	19	96	1266
AYW	AHLSLAGLPV	51	10	18	06	1267
AYW	AKSVOHLESL	546	10	17	85	1268
AYW	ARDVLCLRPV	12	10	15	7.5	1269
AYW	ARVTGGVFLV	356	10	60	06	1270
AYW	EHCSPHHTAL	46	10	20	100	1271
AYW	FRKIPMGVGL	501	10	16	08	1272
AYW	FRKLPVNRPI	809	10	9	08	1273
AYR	GRETMENLV	140	10	<del>.</del>	7.5	1274
AYW	HHTALROAIL	51	10	61	56	1275
AYW	HKVGNFTGLY	54	10	61	50	1276
AYW	KRWGYSLNFM	576	10	17	85	1277
AYW	LHLYSHPIIL	490	10	16	80	1278
AYW	LHPAAMPHLL	428	10	20	100	1279
AYW	LHTLWKAGIL	148	10	50	100	1280
AYR	LKLIMPARFY	107	10	15	7.5	1281
AYW	LARFIIFLFI	.240	10	15	7.5	1282
AYW	NKTKRWGYSL	573	10	15	7.5	1283
AVW	NARVAEDLNL	34	10	17	28.55	1284
AYW	PHHTALROAI	50	10	20	100	1285
AVW	PHLIVGSSGL	434	10	16	08	1286
W.A	A SOLICIANO	603	01			1001
===		040	>-		0.5	1071

Avv         Requence         Position in Position in Play         No. of Amino Addiss Anno Addiss Anno Addiss Anno Addiss Anno Addiss Anno Brancheller 5.27         10           Avv         FRAFIEFEIL         24.1         10           Avv         FRAFIEFEIL         24.1         10           Avv         FRAFIEFEIL         24.1         10           Avv         FRAVGNFTGL         5.3         10           Avv         FRILTIPOSL         12.0         10           Avv         VFFASPHAVA         81.9         10           Avv         VFFASPHAVA         38.19         10           Avv         VFFASPHALA         3.26         10           Avv         VFFASPHALA         3.26         10           Avv         VFFASPHALA         3.26         11           Avv         VFFASPHALA         4.8         11           Avv         VFASPHALA         2.26         11           Avv         VFASPHALA         2.26         11           Avv         VFASPHALA         2.0         11           Avv         PHATALLORIA         3.5         11           Avv         PHATILLORIA         2.0         11           Avv         PRAVIARI	No. of Sequence Amino Acids Frequency 10 17 10 19 10 19 10 19 10 19 10 10 10 10 10 10 10 10 10 10 10 10 10 10 11 11 11 11	Conservancy (%) (%) 85 95 75 85 95 85 95 86	SeqID Num 1289 1290
RRYTSFPWL RRAFPHCLAF RRFIIFFIL SRIVATSFPWL SRIVATSFPWL SRIVATSFPWL SRVAVBSGF THVGANFTGL TRYLPLDKGI TRYLPLCG TRYLPCG TRYLPC		85 95 75 85 95 85 100 80	1289 1290
RRAFPHCLAF  RRFIIFLEL  SRKYTSFWUL  SRKYTSFWUL  STANUTOSQF  TRILITIOQSL  VRFSWLSLIV  VRFSWLSLIV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  VRFSWLSLV  SS  VRFSWLSLV  VRFSWLSLV  SS  VRFSWLSLV  VRFSWLSLV  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  SS  VRFSWLSC  VR		95 95 85 95 95 100 80	1290
RRFIIFLFIL SRKYTSFPWL SRKYTSFPWL SRKYTGFPWL SRKYTGFPWL SRKYTGFWL STA THILTIPOSL THILTIPOSL WKVCGNFUCL WKWCGNFUCL	75 85 95 95 100 80		
SRIVINGEOF 375  THIVORNITGI. 53  THIVORNITGI. 53  THIVORNITGI. 575  THILTIPOSI. 120  THILTIPOSI. 186  WHILTIPOSI.	85 95 95 100 80	1291	
SRLWDFSQF 375  THYCAMPTGL 53  THYCAMPTGL 53  TRYLPLDKGI 120  TRILITROSIL 120  WHFASPLHVA 819  WHFSWLSLLV 526  WHCAPHCLA 526  WHCASPHUNAW 609  SRCTSFWLL 241  WHCAPHCLA 526  WHCAPHCLA 526  WHCAPHCLA 526  WHCAPHCLA 526  WHCAPHCLA 526  WHCAPHCLA 526  WHCAPHCLA 526  WHCAPHCLA 526  WHCAPHCLA 526  WHCAPHCLA 526		95 95 85 100 80	1292
THKVGNFTGL 53  TKRWGYSUNF 575  TKYLPLDKGI 120  TRILTIPOSL 186  WHFSWLSLLV 331  WRAPEPHCLA 526  WKVCORNGL 619  YRWMCLRAFI 235  DHGALLAACF 619  WKVCORNGL 55  LHARMPHLLV 148  LHARMPHLLV 148  LHARMPHLLV 50  PHYTALROAL 50		95 85 100 80	1293
TKRWGYSUNF 575  TKYLPLDKGI 120  TRILTIPOSL 186  VHFASPLHVA 819  VRFASPLHVA 819  VRFASPLHVA 819  VRAKPHCLA 619  VRAKPHCLA 619  VRAKCORNCIL 619  VRAKCORNCIL 619  VRAKCORNCIL 619  VRAKACIL 714  LHPARLLACF 714  LHPARLLACF 714  LHTALLACF 714  LHTALLACF 714  LHTALLACF 714  LHTALLACF 714  LHTALLACF 714  LHTAKLACH 55  LHTALLOAIL 55  LHTALLOAIL 50  PKFAVRHUCSL 90  PRTAPANTGGV 623  RKLPVIRRIGL 90  PRTPANTGGV 623  RKLPVIRRIGL 654  RKLPVIRRIGL 654  RKLPVIRRIGL 654  RKLPVIRRIGL 654  RKLPVIRRIGL 654  RKLPVIRRIGL 654  SAQCGWLWGM 699  RRHILLINKA 105  SRKYTSFPWLL 743  THKWGYSLNFM 575  TRRWGYSLNFM 619  VRRAFSPLLVAW 819  VRRAFSPLLVAW 619		85 100 80	1294
TRILTIPOSL  WH-ASPLHVA  WH-ASPLHVA  WR-SPLHVA  WR-SPLHVA  WR-CLARFI  WR-CLARFI  DH-GA-LSLRGL  WANDCHRFI  DH-GA-LSLRGL  WANDCHRFI  DH-GA-LSLRGL  WANDCHRFI  DH-GA-LSLRGL  WANDCHRFI  DH-GA-LSLRGL  WANDCHRFI  DH-GA-LSLRGL  WANDCHRRGL  DH-GA-LSLRGL  WHTALHOAL  BRFIIFLR  BRANCHGRA		100 80	1295
TRILTIPOSL 186  WHFASPLHVA 819  WHFASPLHVA 819  WRASPLHVA 819  WRASPLHVA 819  WRASPLHVA 819  WRASPLHCIA 826  HTAELLAACF 714  LHTAELLAACF 714  WHTALROALF 85  LHTAMAGAILY 148  LHANDWITTARW 148  WRANDWILGFAA 623  GRINGLLGFAA 623  GRINGLLGFAA 623  GRINGLLGFAA 623  RKLPVNRPIDW 609  RRFIILCFILL 241  RRLKINARF 105  SACOLGWLWGM 20  SRKYTSFPWL 743  THRVGNFTGLY 53  TRAWGYSLNFM 819  WRANDGRINGL 526  WRANDGRINGL 619		80	1296
WHFASPLHVA         819           WRFSWLSLLV         331           WRRAFPHCLA         526           WKOCARIVGL         619           YRWMCLARFI         235           DHGAPLIGGL         48           IHLNPAMPHILV         428           IHTAELLAACF         714           LHTWAGILY         428           LHTWAGILY         55           LHTWAGILY         56           PHHTALOALL         50           PKANLOGIL         623           PKANLOGIL         623           PKANLOGIL         623           PKANLOGIL         623           PKANLOGIL         63           SKYTSFPWIL         743           TRAWGYSLIMM         614           WHASPPHCLAF         526           WANCOGRIGIL         619			1297
VRFSWLSLLV         331           VRRAFPHCLA         526           WKVCORNGL         619           YRWMCLBRFI         235           DHGALSLRGL         48           IHTABLLAACF         714           IHTABLLAACF         714           LHTAKAGILY         428           LHTAKAGILY         148           LPHAMPHILLV         428           LHTAKAGILY         148           LPRFIIFLFIL         240           PHTALARAGILY         394           PKFAVPNICGL         39           PRTPARYIGGL         35           ORIVGLIGFA         623           RKLPVNRPIDW         609           RRLIFIFLIL         241           RRLIGFRKI         20           SHPIILGFRKI         494           SACCGWLWGM         20           SRYTSFWIL         743           THWKGNFTGLY         53           TRHYGNFTCLY         53           TRHYLLINKA         144           WHASPLHYLAR         526           WANVCORINGL         619		80	1298
WKVCQRVGL         526           WKVCQRVGL         619           YRWMCLRFF         235           DHGALLSLRGL         48           IHTAELLAACF         714           IHTAELLAACF         714           LHPAAMPHLV         428           LHTWKAGILY         148           LHAAMPHLV         428           LHTWKAGILY         148           LPRFIIFLFIL         240           PHHTALROAIL         50           PKAVPINICOSL         394           PKTAVRIGGV         352           ORIVGLGFAA         623           RKLPVNRPIDW         609           RRLIELFILL         241           RRLIELFILL         241           RRLIELFILL         241           RRLINGGRY         55           SHPILGFRKI         494           SACGGWLWGM         20           SRYTSFWILL         743           TRHVGNYSLUFM         57           TRHYCHTLWKA         819           VHFASPLHCLAF         526           WANVCORIVGL         619		. 80	1299
WKVCQRIVGL         619           YRWMCLRRFI         235           DHGAHLSLRGL         48           IHLINPINTKRW         568           IHTAELLAACF         714           LHAAMPHLLV         428           LHTUMKAGILY         428           LHTUMKAGILY         148           LPRFIIFLFIL         240           PHHTALROAIL         50           PKFAVPNICOSIL         394           PKTAVPNICOSIL         394           PKTAVPNICOSIL         394           PRTPARAVIGGV         352           QRITPARAVIGGV         352           QRITPARAVIGGV         352           ARL PVNNRPIDW         609           RRL LILL         241           RRL LILL         241           RRLIELFILL         241           SRCGGWLWGM         20           SRKYTSFPWLL         743           THKVGNFTGLY         53           TRHYLLINKA         144           VHFASPLLAR         526           WANYCORIVGL         526           WANYCORIVGL         619		95	1300
YRWWCLRFI         235           DHGAHLSLRGL         48           IHLNPNKTKRW         568           IHTAELLAACF         714           LHPAAMPHILV         428           LHAAMPHILV         428           LHAZILAGILY         148           LRAPIILFIL         240           PHYALKINGAL         50           PKAVPRICOSL         394           PKAVPRICOSL         394           PKAVPRICOSL         360           PRYLHKTLGL         90           PRTPARVIGGV         352           QRIVGLGFAA         623           RKLPVNRPIDW         609           RRLIGFRIL         241           SRCGGALWGM         20           SRCCGALWGM         20           SRCCGALWGM         53           THKVGNSTGLY         53           TRHYLHTLWKA         144           VHFASPLHCLAF         526           WANCORINGL         619		85	1301
DHGAHLSLRGL IHLNPNKTKRW IHTAELLAACF LHPAAMPHLLV LHTLWKAGILY LHOALCWGEL LRAFIIELFIL PHATALROAIL PKYLHKRT.GL PRTPARVTGGV QRIVGLGFAA RKLPVNRPIDW RRFIIELFILL RRIKLIMPARF SHPIII.GFRKI SKQ.CGWLWGM SRKYTSFPWLL THKVGNFGLY TKRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRPAFPHCLAF	11 19	95	1302
IHLNPNKTKRW IHTAELLAACF LHPAAMPHILV LHTAWKAGILY LROALCWGEL LRFIIFLFIL PHTFALROAIL PKTAVPULQSL PKYLHKRTGL PRTPARVTGGV QRIVGLIGFAA RKLPWNRPIDW RRFIIFLFILL RRFIIELFILLFILLFILL RRFIIELFILLFILLFILLFILLFILLFILLFILLFILLFIL	11	95	1303
IHTAELLAACF LHPAAMPHLLV LHTWKAGILY LDAALCWGEL LRFIIFLFIL PHTALROAIL PKYAVPNLGSL PKYLHKRTGL PRTPARVTGGV QRIVGLGFAA RYLPVNRPIDW RRFIIFLFILL RRLIMPARF SHPIIGFRKI SYLCGWLWGM SRKYTSFPWLL THKVGNFGLY TRRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRPAFPHCLAF		7.5	1304
LHPAAMPHLLV LHTWKAGILY LHOALCWGEL LREFIIFLFIL PHTALROAIL PKFAVPNLOSL PKTPARTGGL PRTPARTGGV ORIVGLIGFAA RRLPVNRPIDW RRFIIFLFILL RRLIMPARF SHPIIGFRKI SRQCGWLWGW SRRYTSFPWLL THKVGNFTGLY TRRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF	11 17	85	1305
LHTLWKAGILY LARFIIFLFIL PHHTALROAIL PHTALROAIL PKFAVPNLOSL PRTPARYTGGV ORIVGLLGFAA RRLPVNRPIDW RRFIIFLFILL RRLIKLIMPARF SHPIIGFRKI SRQCGMLWGM SRKYTSFPWLL THKVGNFTGLY TRRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF	11 17	85	1306
LROAILCWGEL LRAGIL PHHTALROAIL PHTALROAIL PKFAVPNLOSL PRTPARVTGGV ORIVGLIGFAA RRLPVNRPIDW RRIPLFILL RRLIMPARF SHPILGFRKI SRQCWLWGM SRKYTSFPWLL THKVGNFTGLY TRRWGYSLNFM TRHYLHTLWKA VHRAFPHCLAF WANCORIVGLL	11 20	100	1307
LARFIIFLFIL PHTALROAL PKFAVPNLOSL PKVLHKRTLGL PRTPARVTGGV ORIVGLGFAA RKLPVNRPIDW RRIPLFILL RRLIMPARF SHPIILGFRKI SRQCGWLWGM SRRQTSFPWLL THKVGNFTGLY TRHYLHTLWKA VHRASPLHVAW VRRAFPHCLAF WAVCORIVGLE	11 18	06	1308
PHHTALRGAIL PKRAVPILIOSI. PRYLHKRTLGL PRTPARVTGGV QRIVGLLGFAA RKLPVNRPIDW RRFIIFLFILL RRLIMPARF SHPIILGFRKI SKQCGWLWGM SRKYTSFPWLL THKVGNFTGLY TRRWGYSLNFM TRHYLHTLWKA VHRAFPHCLAF WKVCQRIVGLL	11 15	7.5	1309
PKFAVPNLOSL PRTPARTIGL PRTPARYTGGV ORNGLIGFAA RALEVNNRPIDW RRFIIFFILL RRFIIFFILL RRFIIFFRII SYLOGWWGM SRRYTSFPWLL THKYGNFTGLY TRKWGYSLNKM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WKYCORIVGL	11 19	95	1310
PKYLHKRTLGL PRTPARVTGGV ORNGLLGFAA RRLPUNRPIDW RRFIIF,FILL RRHLIMPARF SHPIILGFRKI SKLCGWLWGM SRRYTSFPWLL THKYGNFTGLY TRKWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WKYCORIVGL	11 19	95	1311
PRTPARVTGGV ORIVGLLGFAA RRLPVNRPIDW RRIPIEFILL RRLIMPARF SHPIILGFRKI SKLCGWLWGM SRKYTSFPWLL THKVGNFTGLY TRKWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WACCORIVGL	11 17	85	1312
QRIVGLLGFAA RYLPVNRPIDW RRIIFILL RRIIFILL RRIILGFRKI SYLCGWLWGM SRYTSFPWLL THYVGNFTGLY TRYWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRPAFPHCLAF WAVCQRIVGLL	11 18	06	1313
RKLPVNRPIDW RREIIFLIL RREIIGFRII SHQUGGMUGGM SRRYTSFPWLL THKVGNFTGLY TRRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WAVCORIVGLL	11 18	06	1314
RREIFLELL RRLIMPARF SHPILGFRKI SKQCGWLWGM SRKYTSFPWLL THKVGNFTGLY TKRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WAVCORIVGLL	11 16	80	1315
RRLKLIMPARF SHQGENLY SHCYTSFWLL THKVGNFTGLY TKRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VHRAFPHCLAF WAVCORIVGLL	11 15	7.5	1316
SHPIILGFRKI SRCA.GWLWGM SRKYTSFPWLL THKVGNFTGLY TKRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WAXVCQRIVGLL	11 15	7.5	1317
SKCCGWLWGM SRKYTSFPWLL THKVGNFTGLY TKRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WAYCCORIVGLL	11	80	1318
SRKYTSFPWLL THKVGNFTGLY TKRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WAVCQRIVGLL	11 17	85	1319
THKVGNFTGLY TKRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WAVCORIVGLL	11 17	85	1320
TKRWGYSLNFM TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WAVCORIVGLL	11 19	9 6	1321
TRHYLHTLWKA VHFASPLHVAW VRRAFPHCLAF WAYCCORIVGLL	11 17	85	1322
VHFASPLHVAW VRRAFPHCLAF WAYCCORIVGLL	11 20	100	1323
VRRAFPHCLAF WKVCQRIVGLL	11 16	80	1324
WKVCQRIVGLL	11 19	95	1325
	11 17	85	1326
YRWMCLRRFII	11 19	95	1327

TABLEX

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	SEQ ID NO:	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373
	Conservancy (%)	85	85	100	06	80	80	92	06	100	92	92	75	82	80	300	95	100	06	98	92	85	06	82	100	100	95	56	95	9 9	n 40	06	100	95	80	100	100	95	80	06	95	06	7.5	82	0 0 1	7.5
	Sequence Frequency	17	17	20	18	16	16	19	18	. 50	19	19	15	17	9	6.	<u>6</u>	20		19	19	17	18	17	20	50	6.	6	9	0.7	71	81	. 20	19	16	20	20	19	16	18	19	48	15	17	16	٦ <b>٥</b>
Motif	No. of Amino Acids	60	80	80	8	œ	80	80	80	ဆ	æ	æ	∞	œ	∞ ⋅	ao e	<b>x</b> 0 '	<b>~</b>	<b>&amp;</b>	ထ	<b>~</b>	∞ ·	ထ	<b>6</b> 0 (	<b>&amp;</b>	<b>20</b> (	∞ (	<b></b>	<b>x</b> 0 0	ο α	<b>)</b> 60	· 60	<b>co</b>	80	80	æ	&	æ	æ	బ	æ	æ	æ	<b>∞</b>	<b>ω</b> (	ĸ
HBV B58 Super Motif	Position	431	. 46	166	19	822	329	069	69	48	523	374	142	724	821	658	63	333	536	635	518	545	735	715	52	149	515	45	415	500	742	408	412	108	103	136	430	641	=	355	130	779	692	797	15	351
	Sequence	AAMPHLLV	ASALYREA	ASFCGSPY	ASKLCLGW	ASPLHVAW	ASVRFSWL	ATPTGWGL	CALRFTSA	CSPHHTAL	CSWRRAF	ESPLWDF	ETVLEYLV	FARSRSGA	FASPLHVA	TSP17KAF	FSSAGPCA	FSWLSLLV	FSYMDDVV	FTQCGYPA	FTSAICSV	GAKSVOHL	GTDNSWL	HTAELLAA	HTALROAL	HILWKAGI	LACHISAL	ייטאייאיי	LSLDVSAA	LSLEVITY ISLBGI PV	LSRKYTSF	LSSNLSWL	LSWLSLDV	LTFGRETV	MSTTDLEA	NAPILSTL	PAAMPHLL	PALMPLYA	PARDVLCL	PARVTGGV	PAYRPPNA	PSRGRLGL	PTGWGLAI	PITGRISE	PIVOASKL	FIVWLSVI
Table XIII	Protein	ğ	NC	ಜ	SP	젍	2	<u>ಕ</u>	×	2	ಕ :	호 :	3 X	로 1	컾 :	₹ >	× ;	≩ 8	로 :	ਫ਼ :	로 1	젍 :	<u>ਵ</u>	₫ :	2 2	₹ 8	로 :	3	ᅻ 8	×	. ජ	ಶ	젒	- NC	×	2	ğ	ප්	×	ಶ	2		ರ :	<b>ਰ</b> ੇ	2 2	<b>2</b>

RAFPHCLA RTLGLSAM		Suillo Acids	riequency		
TLGLSAM	528	8	19	95	1374
	96	80	24	120	1375
SALYREAL	35	æ	18	06	1376
SSAGPCAL	64	8	19	95	1377
SSGTVNPV	136	ထ	15	75	1378
SSKPROGM	ĸ	œ	18	06	1379
STLPETTV	141	ထ	20	100	1380
STTDLEAY	104	æ	15	75	1381
TALROAIL	53	8	. 61	92	1382
TSAICSVV	519	80	19	95	1383
TSGFLGPL	168	80	16	80	1384
TTDLEAYF	105	80	15	75	1385
TTGRTSLY	798	80	17	85	1386
VSWPKFAV	391	•	19	56	1387
NSVVNVM	115	) ac	0 0	501	1388
VTGGVE V	 		2 6	8 6	1380
WSPOADG	9 9	<b>α</b>	2 -	2 e	0000
WHINGNE	9 c		- 6	5	1000
VC) NEWCO	32	<b>.</b>		001	- 000
VISEDMI	346	οα		n u	1392
AABETOCOV	740	ത ര		0.0	2000
ASAL VBEAL	932	n c	. ·	n u	400
ASKI CI GWI	) + (	n o	~ œ	6 6	1396
ATPTGWGLA	6-8	ით	9 5	08	1397
CSRNLYVSL	471	, on	16	90	1398
DATPTGWGL	089	, on	6	5 G	1399
DSWMTSLNF	196	თ	19	56	1400
EAGPLEER	17	6	20	100	1401
FADATPTGW	687	6	19	96	1402
FASPLHVAW	821	თ	16	80	1403
FAVPNLOSL	396	6	19	92	1404
FSPTYKAFL	658	თ	19	95	1405
FSSAGPCAL	63	O	19	95	1406
FSYMDDVVL	536	6	18	06	1407
FTFSPTYKA	656	6	19	95	1408
FTGLYSSTV	59	თ	18	90	1409
FTOCGYPAL	635	6	19	95	1410
FTSAICSVV	518	6	19	95	1411
GAHLSLRGL	50	o	19	95	1412
HTALBOAIL	20.00	ത	19	. G	1413
HTLWKAGIL	149	o	20	100	1414
KSVOHLESL	547	6	17	85	1415
KTKRWGYSL	574	6	19	95	1416
LAFSYMDDV	534	6	18	06	1417
LSFLPSDFF	45	ത	19	56	1418
SIDVSAAF	2 - 7	σ	0	40	1419

HBV B58 Super Motif

Table XIII

	SEQ ID NO:	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	7 4 7	1445	1446	1447	1448	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465
	Conservancy (%)	95	7.5	100	7.5	7.5	7.5	06	82	75	06	82	06	 	7.5	95	06	080	36	080	06	001	90	. 60	5 5	. 60	80	80	7.5	85	100	85	06	80	. 75	100	85	80	75	92	100	80	80	06	80	96 .
	Sequence Frequency	19	15	20	15	15	15	18	17	15	<b>6</b>	17	<b>8</b>	17	3.	<b>Б</b> .	æ '	9 ,	9 ,	9.	 	07 7	D 14	n c	07	17	16	16	15	17	20	17	18	16	15	20	17	16	. 15	19	20	16	16	18	9 :	19
uper Motif	No. of Amino Acids	6	6	6	. 6	6	6	6	6	6	<b>o</b>	<b>6</b>	<b>o</b>	<b>o</b> n (	ത	<b>න</b> (	ത	<b>a</b> n (	<b>.</b>	<b>.</b>	ത	en c	on c	n c	ை	ກອ	ത	တ	6	6	6	6	6	6	<b>o</b>	10	10	10	10	10	10	10	10	10	0	10
HBV BS8 Super Moti	Position	510	349	140	16	ო	137	404	66	103	738	430	355	797	351	654	57	18	528	167	က် ်	165	904	135	141	. 407	) (C	764	168	798	48	99	4	493	580	166	19 •	329	069	61.	310	298	689	196	32	631
	Sequence	LSPFLAOF	LSPTVWLSV	LSTLPETTV	LSVPNPLGF	LSYOHFRKL	LTFGRETVL	LTNLLSSNL	LTVNEKRRL	MSTTDLEAY	NSVVLSRKY	PAAMPHLLV	PARVIGGVE	PITGRISLY	PIVMLSVIW	CAFIFSPIY	OALCWGEL OAGG COM	OASKLCLGW	HAFPHCLAF	HIGDPAPNM	SAGPCALRE	SASFCGSPY	SSINCSWEST	A-NN-15000	STEPETIVE .	TAFLLACE	TASALYBEA	TSFVYVPSA	TSGFLGPLL	TTGRTSLYA	VSIPWTHKV	WSPOAGGIL	WSSKPROGM	YSHPIILGF	YSLNFMGYV	ASFCGSPYSW	ASKLCLGWLW	ASVRFSWLSL	ATPTGWGLAI	CAFSSAGPCA	CTCIPIPSSW	CTIPAGGTSM	DATPTGWGLA	DSWWTSLNFL	DTASALYREA	FAAPFTOCGY
Table XIII	Protein	Σ	M M	3	M M	젍	3		젙	×	쥖 :	<b>2</b> 1	ರ :	<b>z</b> ?	≩ 8	호 :	3 2	3 8	₹ 8	<b>≩</b> ;	×	로 8	₹ 8	è 2	} >	۲ ۾	3 3	ಕ	<b>₩</b>	젍	젍	26	2	젍	ಕ	ದ್ದ	SZ.	<u>~</u>	ದ	×	26	8	젍	2	2	젍

	SEQ ID NO:	1466	1467	1468	1469	1470	1471	1472	1473	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1488	1489	1490	1491	1492	1493	1494	1495	1496	1496	1499	1500	1501	1502	1503	1504	1505	1506	1507	1508	1509	1510	
	Conservancy (%)	100	95	190	7.5	75	80	82	100	מ מ	100	95	75	85	06	100	100	75	06	٠ د د	) 6	9 6	75	06	95	82	80	150	80	180	0 0	06	06	92	06	85	95	80	7.5	. 08	7.5	35 6	75 85	
	Sequence Frequency	20	19	38	15	15	9 ;		100 100 100 100 100 100 100 100 100 10		20	19	15	17	18	20	20	15	æ :	<u>.</u>	ο α 	o 6-	15	18	19	17	16	30	16	36	D 4		18	19	18	17	19	16	15	16	15	6 :	15 17	
Motif	No. of Amino Acids	10	10	10	10	0 :	<u></u>	2 9	0 4	2 5	2 0	÷ 2	10	10	10	10	10	9	0,	0 9	2 -	2 0	0+	10	10	10	10	0 :	10	0 ;	2 5	2 0	10	10	10	. 10	10	10	0	10	10	10	- 10	
HBV B58 Super Motif	Position	333		635	134	13	763	715	149	0.00 1.11	336	53	349	742	408	140	412	က	189	103	131	641	145	355	130	797	15	351	179	57	/O1	193	353	520	64 *	716	53	33.	747	764	168	37	580 721	
	Sequence	FSWLSLLVPF	FTFSPTYKAF	FTOCGYPALM	GSSSGTVNPV	GINLSVPNPL	GTSFVYVPSA	HIAELLAACE	HILWKAGILY LAFOXMODAV	I SI DVSAAFY	LSLLVPFVQW	LSLRGLPVCA	LSPTVWLSVI	LSRKYTSFPW	LSSNLSWLSL	LSTLPETTW	LSWLSLDVSA	LSYOHFRALL	LIPOSLDSW	DADOSEDE	PADDPSHGAL	PALMPLYACI	PAPCNFFTSA	PARVTGGVFL	PAYRPPNAPI	PTTGRTSLYA	PTVQASKLCL	PTVWLSVIWM	QAGFFLLTRI G.:: 2::05	OAILCWGELM	SANCE CHARGO	OSLDSWMTSL	RTPARVTGGV	SAICSVVRRA	SSAGPCALRF	TAELLAACFA	TALROALCW	TASALYREAL	TSFPWLGCA	TSFVYVPSAL	TSGFLGPLLV	VAEDLNLGNL	YSLNFMGYVI AACFARSRSGA	
Table XIII	Protein	BW	전	전 :	<b>&amp;</b> ∂	£ 8	ಕ ಚ	₹ 8	ಕ ಜ	d 2	<b>2</b> 60	×	AG	තු		SZ :	ಕ :	로 ?	≩ >	≺ ≿	₫ &	: Z	×	&	<b>27</b>	ರ :	2	<b>&amp;</b> i	<b>M</b> :	3 2	) I	Ma	ğ	점	×	전	ST ST	3	<u>ಕ</u>	전	<b>S</b>	₹ 9	로 로	

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	SEQ ID NO:	1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1524	1525	1526	1527	1528	1529	1530	1531	1532	1533	1534	1535	1537	1538	1539	1540	1541	1542	1543	- 5044	1546	1547	1548	1549	1550	1551	1552	1553	1554	1555	1557
	Conservancy (%)	95	80	98	130	100	100	7.5	80	95	500	G Ç	8 6	9 6	. 06	. 82	80	85	95	06	82	06	95,	00 4 6	, c	92	95	7.5	7.5	06	06	80	C 6	95	140	95	80	7.5	06	92	06	ດ	100
	Sequence Frequency	19	16	19	26	20	50	15	16	19	6 °	8 C	2 6	- <del>-</del>	81	17	16	17	19	8 .	17	8 :	19	07	. <del>.</del>	17	- 19	15	15	18		0 1	. <del>.</del>	6-	28	19	16		18	19	18	5 (F	20
<u>Motif</u>	No. of Amino Acids	11	Ξ	Ξ	=	=	Ξ	=	Ξ	Ξ	= ;	= ‡	- ‡	= =	Ξ	Ξ	Ξ	=	=	=	Ξ	= :	= ;			= =	Ξ	Ξ	Ξ	=	••• ;	= ;	= =	=	=	=	=	=	=	7	= :	Ξ;	= =
HBV BS8 Super Motif																																											
	Position	632	329	61	69	48	310	689	32	374	687	63	555	9.56 6.56	20	545	763	715	52	105	574	. 534	515	336	0.00	742	412	ິ ຕ	137	189	404	185	355	130	351	654	179	18	402	528	353	127	520 165
	Sequence	AAPFTOCGYPA	ASVRFSWLSLL	CAFSSAGPCAL	CALRFTSARRM	CSPHHTALROA	CTCIPIPSSWA	DATPTGWGLAI	DTASALYREAL	ESPLWDFSQF	FADATPTGWGL	FORM OF LABOR	ESYMODIVALGA	FTESPTYKAFL	GAHLSLRGLPV	GAKSVOHLESL	GTSFVYVPSAL	HTAELLAACFA	HTALROAILCW	ISCLIFGRETV	KTKRWGYSLNF	LAFSYMDDVVL	LAGETSAICSV	LSLLVPTVCWF	SPACE SON	LSRKYTSFPWL	LSWLSLDVSAA	LSYOHFRKLL	LTFGRETVLEY	LTIPOSLDSWW	LTNLLSSNLSW	LI MIL IIPUSL BABDA CI BBA	PARDYLCLAP	PAYRPPNAPIL	PTVWLSVIWMM	OAFTFSPTYKA	OAGFFLLTRIL	OASKICLGWLW	OSLTNLLSSNL	RAFPHCLAFSY	RTPARVTGGVF	HIPPAYHPNA	SAICSVVHHAF SASFCGSPYSW
Table XIII	Protein	ğ	<b>№</b>	×	×	3	BN BN	젍	3	⊈ :	ರ >	< 8	ā &	් ද	×	گ	ಜ	ಕ	3	3	ರ -	젇 :	ಕ ಕ	} >	< 6	දූ ද	<u>්</u> ද	젒	3	AB A	점 :	A >	٠ <del>۵</del>	2	26	젒	<b>№</b>	2	젙	್ಷ	젍 :	3	호호

Table XIII		HBV B58 5	HBV B58 Super Motif				
Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:	
ಜ	SSNLSWLSLDV	409	11	18	06	1558	
젍	TSAICSVVRRA	519	11	19	95	1559	
젍	TSFPWLLGCAA	747	1	15	75	1560	
26	TSGFLGPLLM	168	=	15	7.5	1561	
젍	VSWPKFAVPNL	391	11	19	95	1562	
젍	WTHKVGNFTGL	52		19	95	1563	
Š	YTSFPWI I GCA	746			7.5	1564	

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Table XIV

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SEQ ID NO:	1565	1566	1567	1568	1569	1570	1571	1572	1573	1574	1575	1576	1577	1578	1579	1580	1581	1582	1583	1584	1585	1586	1587	1588	1589	1590	1591	1592	1593	1594	1595	1596	1597	1598	1599	1600	1601	1602	1603	1604	1605	1606	1607	1608	1609	1610	1611
Conservancy (%)	06	95	95	100	82	100	92	85	06·	85	80	06	98	80	06	80	80	7.5	95	7.5	95	95	06	95	100	06	95	80	80	100	80	80	06	100	08	95	100	06	80	06	80	85	7.5	80	95	85	100
Sequence Frequency	18	19	19	20	17	. 20	19		18	17	16	18	19	16	18	16	16	15	19	15	19	19	18	19	20	18	19	16	. 9	20	16	16	. 8	50	9 :	5	20	18	16	18	16	17	15	16	19	17	20
No. of Amino Acids	8	89	89	<b>ထ</b>	жо (	ao (	<b>x</b> 0 ·	ω	8	80	బ	80	89	89	80	80	80	80	80	80	8	8	8	<b>60</b>	89	ဆ	8	8	∞ :	æ	<b>co</b> ·	œ ·	<b>~</b>	<b>20</b> (	æ (	<b>x</b> 0 (	<b>20</b> (	<b>x</b> 0 ·	œ	8	æ	89	89	80	80	80	80
Position	58	633	397.	312	23	253	239	622	31	59	122	33	14	122	718	243	248	171	256	749	346	342	166	509	348	. 265	173	207	491	429	244	497	28	249	200	188	313	191	315	625	503	21	108	610	55	91	254
Sequence	ALCWGEL	APFTQCGY	AVPNLOSL	CIPIPSSW	CLGMLWGM	CLIFILVI	CLRRFIIF	CORINGLL	DIDPYKEF	DLLDTASA	DPRVRGLY	DPYKEFGA	DVLCLRPV	PLGEERL	ELLAACFA	FIIFLFIL	FILLICLI	RGPLLYL	FLIVLDY	FPWLGCA	FVGLSPTV	FVOWFVG	FVYVPSAL	GLSPFILA	GLSPTVWL	GMLPVCPL	GPLLVLOA	GVGLSPFL	HLYSHPII	HPAAMPHL	IIFLFILL	IILGFRKI	ILCWGELM	ILLCLIF	ILRGTSFV	LTIPOSL	IPIPSSWA	POSLDSW	IPSSWAFA	IVGLLGFA	KIPMGVGL	KLCLGWLW	KLIMPARF	KLPVNRPI	KVGNFTGL	KVLHKRTL	UFLLVL
Protein	NC	ದ		<u>~</u>	S :	<b>%</b>	<b>8</b>		3	2	<b>₩</b>	3	×	×	젍	8	8	2	8	젍	8	NA NA	<u>ಜ</u>	젍	· All	<b>8</b>	BN BN		ಶ	ೱ	26		2	<b>%</b>	<b>#</b> 1	<b>A</b>	<b>8</b>	<b>8</b>	<b>№</b>	전	<b>હ</b>	<b>S</b>	젒	전	젍	×	NB.

SEQ ID NO:	1612	1613	1614	1615	1616	1617	1618	1619	1620	1621	1622	1623	1624	1625	1626	1627	1628	1629	1630	1631	1632	1633	1634	1635	1636	1637	1638	1639	1640	1641	1642	1643	1644	1645	1646	1647	1648	1649	1650	1651	1652	1653	1654	1655	1656	1657	1658
Conservancy (%)	100	95	100	85	98	. 80	95	82	100	100	95	06	80	80	95	100	92	100	85	98	100	98	100	06	100	100	. 75	80	56	100	7.5	75	100	82	100	06	95	82	80	06	7.5	100	06	95	80	100	100
Sequence Frequency	20	19	20	17	19	16	19	17	20	20	19	18	16	16	19	20	19	20	17	19	20	19	50	18	20	20	15	16	6	20	15	15	50	17	50	æ :	6.	11,	16	8	15	20	18	19	16	20	20
No. of Amino Acids	8	<b>60</b>	æ	œ	<b>&amp;</b>	ω	œ ·	<b>∞</b> •	<b>80</b> (	<b>60</b>	<b>∞</b> +	∞ ∘	<b>~</b>	ထ	œ ·	œ (	<b></b>	<b>x</b> 0 ·	∞ ∙	<b>∞</b> ∙	<b>∞</b>	œ (	œ (	œ ·	<b>~</b>	80	œ (	<b>&amp;</b>	<b>20</b> (	<b>x</b> 0 (	<b>20</b> (	<b>20</b> (	<b>.</b>	<b>.</b>	<b>3</b> 0 (	σ (	<b>20</b> 0	σ.	<b>ω</b> (	ю (	<b>x</b> 0 (	ထ	æ	8	œ	80	60
Position	109	514	251	30	260	752	628	63	250	378	563	407	184	436	175	338	643	379	712	178	401	176	339	119	377	-	- !	109	45	400	- 15 - 15	571	380	2.7	3.14	192	* 6.0	210	æ (	024	106	133	86	36	818	357	49
Sequence	LIMPARFY	LLAGFTSA	LICUFL	LLDTASAL	LLDYOGML	LLGCAANW	LLGFAAPF	LLGWSPQA	· LLCUFL	· LLPIFFCL	LLSLGIML	LLSSNLSW	LLTRILTI	LVGSSGL	LLVLOAGF	LLVPFVQW	LMPLYACI	LPIFFCLW	LPIHTAEL	LOAGFFLL	LOSLTNIL	LVLOAGFF	LVPFVQWF	LVSFGVWI	· LWDFSQF	MPLSYQHF	MOLPHLOL	MOWNSTTF	NLNVSIPW	NEOSLTNE	NLSVPNPL	NPNKTKRW	PIFFCLWV	PIHTAELL	PIPSSWAF	POSLDSWW	PVCAFSSA	PVNRPIDW	CLDPARDV	RINGLIGF	RLKLIMPA	RPPNAPIL	ROLLWFH	RVAEDLNL	RVHFASPL	RVTGGVF	SIPWTHKV
Protein	ğ	젒	<b>₩</b>	2	8	전		<b>&amp;</b>	<b>&amp;</b>	2	전 :	ಶ	<b>&amp;</b>	ದ್ದ	8	<b>&amp;</b>	ಶ	<b>%</b>	ಕ .	<b>~</b>	ಶ	2	2	<b>3</b>	ಕ :	ಕ	S	2	전 :	쥖 :	<b>2</b>	전 :	<b>2</b> 2	<b>로</b> 2	<b>≥</b> 3	<b>}</b>	× {	ᅻ :	×į	로 :	ರ '	3	<b>SE</b>		ಕ	ಕ	8

HBV B62 Super Motif

Table XIV

POD.         SLDVSAMF         416         8         119         95         165           POD.         SLDVSAMF         511         8         17         95         1650           POD.         SPALACK         511         8         17         85         1650           BW.         SPALACK         511         8         17         85         1650           BW.         SPALACK         512         8         17         85         1650           BW.         SPALACK         513         8         17         85         1661           BW.         SPALACK         17         8         17         85         1661           BW.         SPALACK         739         8         17         85         1661           BW.         SPALACK         739         8         17         85         1661           PM.         TILPETTY         14         8         17         8         167         1661           PM.         TILPETTY         14         8         17         8         167         1661           PM.         TILL         15         8         16         167         167		paranhan		Amino Acids	Sequence Frequency	(%)	SEQ ID NO:
SPRINGEY 581 8 15 SPOUNDE STATEMENT 581 8 15 SPOUNDE STATEMENT 580 8 17 SPOUNDE STATEMENT 580 8 17 SPOUNDE STATEMENT 580 8 17 SPOUNDE STATEMENT 580 8 17 SPOUNDE STATEMENT 580 8 18 SPO	ರ	SLDVSAAF	416	88	19	95	1659
SPOACOLI         511         8         95           SPOACOLI         679         8         17         85           SPOACOLI         659         8         17         85           STYMAR         17         86         95         87           STYMAR         17         8         17         85           SWILSHOT         17         8         17         85           SWILSHOT         1739         8         17         85           SWILSHOT         1739         8         17         85           INVESTION         150         8         17         85           INVESTION         177         8         18         19         95           INVESTION         177         8         18         19         95           INVESTION         177         8         18         19         95	ಠ	SLNFMGYV	581	8	15	75	1660
SPSPEND         67         8         17         85           SPSPENL         88         17         85         75           SPSPSHL         88         17         85         75           SPSPSHL         89         8         17         85           SPSPSHL         89         8         15         75           SPSPSHL         17         85         75         75           SWLSPAY         142         8         15         75           ILWAGAL         150         100         100         100           ILWAGAL         150         100         100         100           ILWAGAL         17         8         15         75           ILWAGAL         17         8         16         95           ILWAGAL         17         8         17         8           ILWAGAL         17         8         16         95           ILWAGALOW         17	ರ	SPFLLAGF	511	æ	19	98	1661
SPENDEHL, 808 8 17 75 8 17 75 8 18 75 75 75 75 75 75 75 75 75 75 75 75 75	≩	SPOAOGIL	67	8	17	85	1662
SPYWALKY 539 8 15 75 75 75 75 75 75 75 75 75 75 75 75 75	ರ :	SPSVPSHL	808	<b>∞</b> :	17	85	1663
SYCHEGE 17 659 8 15 75 75 75 75 75 75 75 75 75 75 75 75 75	≥ .	SPTVMLSV	350	ထ	15	7.5	1664
SUPPLICE SUP	ರ	SPTYKAFL	629	8	19	95	1665
SWALSKY   139   8   17   85		SVPNPLGF	17	8	15	7.5	1666
The property of the control of the	ರ	SVOHLESL	548	œ	17	œ S	1667
TUMKAGIL   142   8   20   100	ರ '	SWLSRKY	739	8	18	06	1668
Thy Middle 150 8 100 100 100 100 100 100 100 100 100	<b>3</b> ;	TLPETTW	142	<b>∞</b> :	20	100	1669
TUCKGLA 691 8 16 75  TUCKGNPAL 636 8 16 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	ರ :	TLWKAGIL	150	<b>ထ</b>	20	100	1670
TPICKWELA 691 B 19 10 10 10 10 10 10 10 10 10 10 10 10 10	<b>≥</b>	TPPHGGLL	57	ထ	15	7.5	1671
TOCGYPAL 636 636 8 119 95 TOCGYPAL 636 8 179 TOCGYPAL 100 8 177 TOCGYPAL 352 8 15 75 75 VLDYGGRPL 177 8 19 95 VLDYGGRPL 177 8 19 95 VLDYGGRPL 177 8 19 95 VLDYGGRPL 177 8 18 18 90 VLGAKSUCL 17 8 18 18 90 VLGAKSUCL 17 8 18 18 90 VLGAKSUCL 17 8 18 18 90 VLGAKSUCL 17 8 18 19 95 VLGAKSUCL 17 8 18 19 95 VLGAKSUCL 17 8 18 19 95 VLGAKSUCL 17 8 18 19 95 VLGAKSUCL 17 8 18 19 95 VLGAKSUCL 17 8 18 19 95 VLGAKSUCL 17 8 18 19 95 VLGAKSUCL 17 8 18 19 95 VLGAKSUCL 17 8 18 19 95 VLGAKSUCL 17 8 18 18 99 VLGAKSUCL 17 8 18 18 99 VLGAKSUCL 18 18 18 99 VLGAKSUCL 18 18 18 99 VLGAKSUCL 18 99 VLGAKSUCL 1	ರ	TPTGWGLA	691	œ	16	80	1672
TVMERRILL TVMERRILL TVMERRILL TVMUSRRILL TVMUSRRILL TVMCGAM TSSS TSSS TSSS TSSS TSSS TSSS TSSS TS	ರ	TOCGYPAL	636	ထ	19	98	1673
VLDVGSM         352         8         15         75           VLDVGSM         259         8         19         95           VLDVGSM         177         8         19         95           VLDAGARY         769         8         18         95           VASALLAP         17         8         18         90           VALGAKSY         542         8         16         80           WLGAKSY         542         8         16         80           WLGAKSY         125         8         16         80           WLGAKSY         125         8         100         95           WLGAKSY         125         8         100         95           WLGAKSY         144         8         100         95           WLSLVPR         147         8         20         100           WLSLVPR         147         8         20         100           WLSLVPR         147         8         10         95           MLCHARLACI         5         8         18         95           ALCHAPLYACI         642         9         19         19         95           ALMONIN	ರ	TVNEKRRL	100	æ	17	85	1674
VLDVOGN         259         8         19         95           VLDVAGFR         177         8         19         95           VPCVARPY         340         8         19         95           VPCAMICAL         17         8         16         80           VOASIGLC         17         8         16         80           VALANEY         542         8         16         80           WILSIDYS         335         8         20         100           WASLUYP         125         8         20         100           WASLUYP         335         8         20         100           WASLUYP         122         8         20         100           VAPLINEY         122         8         20         100           VAPLINEY         122         8         10         90           VAPLINEY         640         8         18         90           VAPLINEY         640         8         19         95           ALROWGELM         54         9         18         95           ALROWICK         54         9         16         95           ALROWICK <td< td=""><td>≥</td><td>TVWLSVIW</td><td>352</td><td>æ</td><td>15</td><td>7.5</td><td>1675</td></td<>	≥	TVWLSVIW	352	æ	15	7.5	1675
VOAGERLA         177         8         19         95           VVPSALNF         769         8         19         95           VPSALNF         769         8         18         90           VOASKICL         17         8         16         80           VOASKICL         17         8         16         80           WIRTPRAY         125         8         16         80           WISLINGS         414         8         20         100           WISLINGS         147         8         20         100           WISLINGS         147         8         20         100           VALINGS         122         8         18         90           VALINGS         147         8         20         100           VALINGS         640         8         18         90           VALINGS         58         9         18         95           ALCONGEM         100<	≩	WLDYQGM	259	80	19	98	1676
VPROWNY         340         8         19         95           VPSALOWRY         769         8         19         95           VOASKUCL         17         8         18         90           VALGAKSY         542         8         16         80           WALGAKSY         125         8         16         80           WALGAKSY         125         8         16         80           WALDASH         147         8         20         100           WASLDVSA         414         8         20         100           WASLDVSA         147         8         20         100           YPALMPLY         640         8         18         16         95           ALMPLYACI         5         8         18         90         16           ALMPLYACI         54         9         18         95           ALMONISTIFICA         102         9         16         95 </td <td>≥</td> <td>VLOAGFFL</td> <td>177</td> <td>æ</td> <td>19</td> <td>98</td> <td>1677</td>	≥	VLOAGFFL	177	æ	19	98	1677
VPSALINRA         769         8         18         90           VOGASKLCL         17         8         16         90           VACGAKSY         542         8         16         80           WILCAKSY         759         8         16         80           WILCAKSTOWSA         414         8         20         100           WILCARPET         237         8         19         95           YLHTUWA         147         8         20         100           YLHTUWA         118         8         19         90           YLHTUWA         51         8         19         90           YLHTUWA         51         8         19         90           YLHTUWA         521         9         19         90           ALLOWGELM         54         9         19         19           ALLOWGELM         58         9         19         19           ALLOWGELM	≥	VPFVQWFV	340	80	19	95	1678
VOASKICL         17         8         16         80           VULGAKSV         542         8         16         80           WILGAKSV         759         8         16         80           WILGAKSY         759         8         16         80           WILGALONSA         414         8         20         100           WASLUNF         335         8         20         100           WALLAREH         237         8         20         100           YALITAWA         147         8         20         100           YALITAWA         147         8         20         100           YALITAWA         147         8         20         100           YALITAWA         148         8         18         95           YALITAWA         54         8         18         16         95           YOHERGLA         58         9         18         95         14           ALROYOREM         54         9         18         95         14           ALROYOREM         54         9         16         95         14           AROWINSTIF         108         9	ರ	VPSALNPA	769	æ	18	96	1679
WILGAKSV         542         8         18         90           WILGAKSY         759         8         16         90           WILGAKSY         125         8         16         80           WILSLOVSA         414         8         20         100           WASLLVPF         235         8         20         100           WASLLVPF         237         8         19         95           VLHTUMSA         147         8         20         100           VALPIDKGI         122         8         20         100           VALPIDKGI         118         8         19         95           ALONGELMA         58         9         19         15         75           ALCOVICKELMA         58         9         19         9         16         9           ALMOMINSTIF         102         9         16	9	VOASKLCL	17	80	16	80	1680
WINTEGESF 759 8 16 80 WISLUNEA 1125 8 19 95 WINCLERF 237 8 8 20 100 WISLUNF 335 8 20 100 WINCLERF 237 8 9 95  YLHTUWKA 1147 8 8 20 100  YLVSFGW 118 8 19 90  YPALIMPLY G 640 8 19 95  ALCWGELM 521 9 19 95  ALCWGELM 642 9 19 95  ALCWGELM 642 9 19 95  ALCWGELM 642 9 19 95  ALCWGELM 642 9 19 95  ALCWGELM 108 9 19 19 95  ALCWGELM 108 9 19 100  CIPICALVIL 253 9 19 19 95  COPROMINITE 102 9 15  ACHREIRL 253 9 19 19  COPROMINITE 107 9 18 19  COPROMINITE 107 9 19  COPROMINITE 107 9 18  COPR	ರ	WLGAKSV	542	∞ .	18	06	1681
WASLDVSA 125 8 19 95 WASLDVSA 1414 8 6 20 100 WASLLVPF 237 8 19 95 WASLLVPF 237 8 19 95 WASLLVPF 237 8 19 95 WASLLVPF 237 8 100 YPALMALY 640 8 18 90 YPALMALY 640 8 19 95 ALCWGELM 521 9 19 95 ALCWGELM 54 9 9 18 95 ALCWGELM 54 9 9 18 95 ALCWGELM 54 9 9 18 95 ALCWGELM 54 9 9 18 95 ALCWGELM 54 9 9 18 95 ALCWGELM 54 9 9 19 95 ALCWGELM 54 9 9 18 90 CIPICAL 253 9 18 90 CIPICAL 253 9 19 90 COPPONSITE 100 CARFIEL 239 9 19 19 90 COPPONSITE 107 CARFIEL 239 9 19 19 90 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 239 9 100 COPPONSITE 107 CARFIEL 230 CARF	ರ !	WILRGTSF	759	<b></b>	16	80	1682
WASILVNSA         414         8         20         100           WASILLVPF         233         8         20         100           WASILLVPF         237         8         20         100           WACHREI         122         8         20         100           YLPLDKGI         122         8         20         100           YLVSFGVW         640         8         18         90           YCM-FRALL         5         8         18         90           ACSVYRRA         521         9         19         95           ALCWGELM         58         9         18         90           ALCWGELM         58         9         18         90           ALROHICW         642         9         18         90           ALROHICW         642         9         18         90           ALROHICW         642         9         18         90           ALROHICW         102         9         18         90           ALROHICW         102         9         16         90           ALROHICW         102         9         15         17           APONIFTSA	3 8	WIRTPPAY	125	<b>.</b>	19	56	1683
WISHLYPF         339         8         20         100           WACJARFI         237         8         20         100           YLHUKKA         122         8         20         100           YLHUKKA         122         8         20         100           YLHUKKA         122         8         20         100           YPALMPLY         640         8         18         90           YPALMPLY         640         8         19         95           YOHFRALL         5         8         19         95           ALCSVYRRA         521         9         18         95           ALLONGELM         54         9         18         95           ALLONGELM         54         9         18         95           ALMPLYACI         642         9         18         95           ALMOMINSTIF         102         9         16         9           AMOWINSTIF         102         9         16         9           AMOWINSTIF         102         9         16         9           AMOWINSTIF         102         9         16         9           CIPITALITY	3	WLSLDVSA	4 (	ים	20	100	1684
WMCJRHPI         237         8         19         95           VLHTLWKA         147         8         20         100           YLPLDKGI         122         8         20         100           YVSFGW         118         8         18         90           YPALMPLY         640         8         19         95           YCHFRQL         5         8         15         75           ACSVYRRA         58         9         19         95           ALROYGELM         58         9         18         90           ALROYGELM         54         9         19         95           ALROYACI         642         9         19         95           ALROYACI         642         9         19         95           ALROAICW         54         9         16         80           AMONNISTIF         102         9         16         80           AMSTTDLEA         146         9         16         75           AMSTTDLEA         146         9         15         75           CHFIFIT         239         9         16         100           CLIFLSWA <t< td=""><td>≥ 3</td><td>WLSLLVPF</td><td>335</td><td>ж (</td><td>20</td><td>100</td><td>1685</td></t<>	≥ 3	WLSLLVPF	335	ж (	20	100	1685
YLHTLWKA         147         B         20         100           YLPLDKGI         122         B         20         100           YLVSFGW         118         B         16         90           YVAHMPLY         640         B         19         95           YQHFRQL         5         B         19         95           ALCSV/RRA         58         9         18         95           ALMPLYACI         642         9         18         95           ALMPLYACI         642         9         19         95           ALMOMICHA         108         9         19         95           AMOWINSTIF         108         9         16         80           AMOWINSTIF         102         9         16         80           AMOWINSTIF         102         9         16         80           AMOWINSTIF         102         9         16         80           ACIFIENT         253         9         20         100           CLIFLIVIL         253         9         20         100           CRAFIEL         23         9         16         90           CPTVOASSKI <td><b>≩</b> ∂</td> <td>WMCLRRFI</td> <td>23/</td> <td><b>.</b></td> <td>19</td> <td>95</td> <td>1686</td>	<b>≩</b> ∂	WMCLRRFI	23/	<b>.</b>	19	95	1686
YAPLDKGI         122         B         20         100           YAPLUKGI         118         B         20         100           YAPALWPLY         640         B         19         95           YOHFRIGL         5         B         15         75           ACSVARA         521         9         19         95           ALMPLYACI         642         9         18         90           ALMPLYACI         642         9         19         95           ALMPLYACI         54         9         19         95           ALMPLYACI         54         9         19         95           AMOWINSTIF         108         9         16         80           AMSTIDLEA         102         9         15         75           APCNFFTSA         146         9         16         80           CIPISSWA         312         9         20         100           CLIFILVIL         253         9         19         9           CLIFILVIL         253         9         19         9           CLIFILITY         23         9         100         100           CRYMWAL	ರ ಕ	YLHILWKA	147	<b></b>	20	100	1687
YOSFGWN         118         8         18         90           YPALMPLY         640         8         19         95           YOHFRAL         5         8         15         75           ALCONGELM         58         9         19         95           ALLOWGELM         58         9         18         90           ALMPLYACI         642         9         18         95           ALMPLYACI         54         9         19         95           ALMPLYACI         54         9         19         95           ALROWINSTIF         108         9         16         80           AMONINSTIF         102         9         15         75           AMCHILLYAL         253         9         15         75           APCNIFITSA         146         9         15         75           APCNIFITAL         253         9         20         100           CIFILLVIL         253         9         19         9           CLIFILINAL         23         9         19         9           CLIFILINAL         23         9         100         100           CRYRWINGT </td <td>J :</td> <td>YLPLDKGI</td> <td>122</td> <td><b>20</b> (</td> <td>50</td> <td>100</td> <td>1688</td>	J :	YLPLDKGI	122	<b>20</b> (	50	100	1688
YPALMPLY         640         B         19         95           YOHERQL         521         8         15         75           ALCSVARA         521         9         18         95           ALCWGELM         58         9         18         95           ALCWGELM         58         9         18         95           ALCWGELM         54         9         18         95           ALCMPLYACI         642         9         19         95           ALMPLYACI         54         9         19         95           AMCHAILLA         102         9         16         80           AMSTTDLEA         102         9         15         75           APCNIFTSA         146         9         15         75           APCNIFTSA         146         9         15         75           CIPILVAL         253         9         20         100           CLIFILVAL         239         9         19         9           CLIFILIA         239         9         19         9           CLIFILIA         107         9         19         100           COSTYOASKIL	<b>3</b> ;	YLVSFGVW	118	<b>80</b>	18	06	1689
VOHERQL         5         15         75           AICSV/RRA         521         9         15         75           ALCWGELM         58         9         18         95           ALLCWGELM         58         9         18         90           ALLCWGELM         54         9         19         95           ALLCWGELW         54         9         19         95           ALLCWGELW         108         9         16         80           ALLCWGELW         54         9         16         80           AMSTTDLEA         102         9         15         75         11           APCWFITSA         146         9         15         75         11           CIPILVIL         253         9         20         100         11           CLIFILVIL         239         9         19         19         100           CLIFILVIL         232         9         19         <	ಶ	YPALMPLY	640	<b>3</b> 00 (	19	98	1690
AICSVVRRA  AICSVVRRA  AILCVGELM  58  9  18  90  18  90  18  90  19  95  11  90  19  95  11  90  10  95  11  90  11  90  11  90  11  10  10  10	ರ ಕ	YOHERKIL	<b>့</b>	<b>.</b>	15	75	1691
ALCWGELM 58 9 18 90 ALCWGELM 58 9 18 90 ALMPLYACI 642 9 19 95 ALMPLYACI 642 9 19 95 AMCHINEA 102 9 15 75 APCNFTSA 146 9 15 75 CIPIPSSWA 312 9 20 100 CLIFLUAL 253 9 20 100 CLRFIIR 239 9 95 CTFGRETY 107 9 18 90 CCFTOASKL 14 9 16 80	ਰ <u>!</u>	AICSVVRRA	521	ກ (	19	95	1692
ALMPLYACI 642 9 19 95 ALROALICW 54 , 9 19 95 ALROALICW 54 , 9 19 95 AMOWNSTTF 108 9 16 80 AMSTTOLEA 102 9 15 75 11 APONTSA 312 9 20 100 CLIFLUAL 253 9 20 100 CLRFIIFL 239 9 19 19 95 CCPTOASKL 14 9 16 80	3 :	AILCWGELM	96	ລາ (	18	06	1693
ALROALICW 54 19 95 11 19 95 11 19 95 11 108 95	ਰ :	ALMPLYACI	642	ກ່	19	92	1694
AMOWNSTR 108 9 16 80 11  AMSTRDLEA 102 9 15 75 11  APONFTSA 146 9 15 75 11  CLIFILAL 253 9 20 100  CLRFIII. 239 9 19  CLRFIII. 239 9 19  CLRFIII. 232 9 10  CONTINUENCE 232 9 100  TO TO TO TO TO TO TO TO TO TO TO TO TO T	3	ALROAILCW	54	<b>a</b>	19	92	1695
AMSTTOLEA 102 9 15 75 11 APONFTSA 146 9 15 75 11 CIPIDSWA 312 9 20 100 11 CLIFILYIL 253 9 20 100 11 CLRFIII. 239 9 19 95 11 CAPTIONACL 232 9 100 110 CONTOURNEL 232 9 100 110	<b>≥</b> :	AMOWNSTTF	901	<b>a</b> n (	16	80	1696
APONFFISA 140 9 15 75 11	<b>×</b> :	AMSTTDLEA	102	<b>.</b>	15	75	1691
CLIFILVIL 253 9 20 100 11 CLIFILVIL 253 9 20 100 11 CLIFILIT 239 9 19 19 95 11 CLIFILIT 239 9 10 100 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 14 9 16 80 11 CPTOASKL 15	× :	APCNFFTSA	0 40	<b>.</b>	15	7.5	1698
CLIRELINI. 233 9 20 100 CLARFIII. 239 9 19 95 CLAFGRETY 107 9 16 80	<u> </u>	CIPIPSSWA	312	<b>.</b>	20	00.	1699
CLAFFIFL 239 95 19	<b>*</b>	CUPULVU	533	m	20	001	1700
CATFGREIV 107 9 18 90 1 CPTYDASKL 14 9 50 10	≥ 9	CLARFIIFL	239	ກ່	19	95	1701
CHYCASKL 14 9 9 16 80	3 2	CLTFGRETV	107	<b>.</b>	18	06	1702
CONTOUR STATE OF THE SECTION OF THE	<u> </u>	CFGYFWMCL	707	n (	07,	00.	50/1
	3;	CPIVGASKL	<u>*</u> •	<b>.</b>	9.	0 9	1704

HBV B62 Super Motif

Table XIV		<u>HBV B62</u>	HBV B62 Super Motif			
Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO:
NLC	DLLDTASAL	29	6	17	85	1706
젚	DUNICALIAN	40	6	19	95	1707
×	DPARDVLCL	0 1	တဖ	16	80	1708
ಕ 8	DPSPGPLG	7/8	<b>o</b> n c	æ ;	0 0	1709
₹ &	DVVLGAKSV	243	n on	9 4	0 6	1710
8	FILLOUF	248	, <b>6</b> 3	9-	80	1712
₩ M	FIFILLOL	246	G	16	80	1713
젍	FLLAQFTSA	513	တ	. 19	95	1714
ಕ್ಷ	FLISLGIM	562	တေ	19	95	1715
2 2	FLLTRILT	183	<b>o</b> n c	9 4	080	1716
<b>₹</b> 8	FPDHOLDPA	4-			) )	1/1/
₫ &	CDANICON	749	n o	5 4	93	1710
2 ≥	FYGI SPTAW	346	ກິດກ	. c	, G	1720
: ಜ	GLCOVFADA	682	<b>O</b> 3	17	8 6	1721
ಧ	GLIGFAAPF	627	6	19	95	1722
<b>₩</b>	GLIGWSPOA	62	O	17	85	1723
ಜ	GVGLSPFLL	202	<b>o</b>	16	80	1724
3	GVWIRTPPA	123	<b>თ</b> (	6 :	98	1725
ರ :	HILVGSSGL	435	<b>o</b> n c	9 9	80	1726
≼ د	HISTRGIPV	32 491	n o	æ •	) ()	1721
2 &	HETSAPIIL LDAAAADLII	429	no	9 0	001	1729
3 &		244	ை	16	80	1730
젍	ILGFRKIPM	498	6	16	80	1731
NA M	ILLICUFL	249	6	20	100	1732
젍	ILRGTSFVY	760	o	16	80	1733
BN BN	IPIPSSWAF	313	6	20	100	1734
<b>№</b>	IPOSLDSWW	191	<b>o</b>	18	06	1735
전 :	IVGLLGFAA	625	on (	18	06	1736
로 1	KLHLYSHPI	20 c	<b>.</b>	5 ·		1/3/
로 8 	KLIMPARFY	100	<b>.</b>		ດ ທ່	1/38
- ₹ &	KVOUHIVGL	955	n on	~ 6	n v	1740
<u> </u>	LAOFTSAI	514	· <b>О</b>	9 -	9 6	1741
<b>8</b>	LICLIFILY	251		20	100	1742
3	LLDTASALY	30	6	17	85	1743
전	LLGCAANWI	752	თ	16	80	1744
<b>₩</b>	LLCLIFL	. 550	თ	20	100	1745
₹	LLPIFFCLW	378	<b>o</b>	20	100	1746
3 8	LISFLPSDF	44	<b>න</b> ර	o •	500	1747
₹ 8	LESSNESWL	47.5	n o	0 0	) 1	1740
<u></u>	L'VLOAGFF I I VPEVOWE	338		50	001	1750
i Z	CSHEMIT	100	თ	18	. 06	1751
<b>8</b>	LPIFFCLWV	379	6	20	100	1752

PCA         Description         Position         No. old sold sold sold sold sold sold sold						
LPHTAELL	Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)
LPVCAFSSA 58 9 19 16		LPIHTAELL	712	6	17	85
LPANEDIDW		LPVCAFSSA	28	တပ	19	95
UNLDOAGNEY   178   19		LPVNRPIDW	611	<b>.</b>	91	08
LUPPACHAPH		LVLDYOGM	176	ന ഠ	5 9	n (
MANNYMORN SECTION OF THE SECTION OF		LVLUAGFFL	339	നത		י
NLGNLWNSI NLGSNLSW NLOSLYNL NLOSLYNL NLOSLYNL NLOSLYNL NLOSLYNL PIECHWY 300 PIECHWY 314 PIECHWY 314 PIECHWY 314 PIECHWY 314 PIECHWY 314 PIECHWY 314 PIECHWY 314 PIECHWY 315 PLUCKGWY 314 PIECHWY 317 PLUCKGWY 317 PLUCKWY 317 PLUCKGWY 317 PLUCKGWY 317 PLUCKGWY 317 PLUCKGWY 317 PLUCKWY 317 PLUCKGWY 317 PLUCKGWY 317 PLUCKGWY 317 PLUCKGWY 317 PLUCKWY 317 PLUCKGWY 317 PLUCKGWY 317 PLUCKGWY 317 PLUCKGWY 317 PLUCKG		MMWYWGPSL	360	o 60	1.	9 80 S2
NULSANLSW 406 9 18  NULSANLSW 406 9 18  NUSSURIL 410 9 20  NUSWISHIN 411 9 18  PIFFCLIWY 380 9 17  PILOFRIGH 496 9 17  PILOFRIGH 496 9 17  PILOFRIGH 496 9 16  PILOFRIGH 124 9 19  PILOFRIGH 124 9 19  PILOFRIGH 124 9 19  PILOFRIGH 124 9 19  PILOFRIGH 124 9 19  PILOFRIGH 124 9 19  PILOFRIGH 124 9 19  PILOFRIGH 129 9 19  PILOFRIGH 8 9 19  PILOFRIGH 8 9 19  PILOFRIGH 8 9 19  PILOFRIGH 187 9 19  PILOFRIGH 8 9 1		NEGNENVSI	42	6	19	95
NLOSLYML		NITSSNITSM	406	О	18	06
NEWLSLDY   11   18   18   18   18   18   18   1		NLOSLTNIL	400	6	20	100
PHECLIMY 380 9 77 70 17 17 17 17 17 17 17 17 17 17 17 17 17		NLSWLSLDV	411	<b>o</b> (	18	06
PHITAELIA PHICAGRAY PHITAELIA PHICAGRAY PLENEMEN PLOKGRAY PLENEMEN PLOKGRAY PLENEMEN PLOKGRAY PLENEMEN PLUNDAGF PLINITAGL J77 PLIPIFCL J77 PLIPIFCL J77 PLOFFCL J7		PIFFCLWVY	380	<b>.</b>	50	100
PIPSSWAFA 314 99 9 16 PIPSSWAFA 124 9 9 16 PLOKGIKPY 20 9 9 16 PLOKGIKPY 20 9 9 16 PLULOAGE 177 9 9 19 PARGALGA 179 9 19 PARGALGA 189 9 19 PARGALGA 189 9 19 PARGALGA 189 9 19 PARGALGA 189 9 19 RACGALGA 189 9 19 RACGALGA 189 9 19 RACGALGA 189 9 19 SLUPENATAL 189 9 19 SLUPENATOR 337 9 20 SLUPENGYN 337 9 9 18 SLUPENGYN 380 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLOW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 18 THOSLDSW 180 9 180 180 THOSLDSW 180 9 180 180 THOSLDSW 180 9 18 THOSLDSW 180 9 180 180 THOSLDSW 180 9 180 THOSLDSW		PIHTAELLA	500		17	90
PLDKGINAFA 124 9 10 10 10 10 10 10 10 10 10 10 10 10 10		PIILGFRKI	0.40	<b>.</b> .	9 7	0.80
PLEKGKRY 124 2 9 9 19 19 19 19 19 19 19 19 19 19 19 19		PIPSSWAFA	7 7	<b>.</b>	٥ -	o ç
PULPIFECL 377 9 9 19 PULPIFECL 377 9 9 19 PULVIOAGE 171 9 9 19 PULVIOAGE		PLDKGIKPY	471	<b>.</b>	0 7	001
PLLYLOGGE 171 9 19 19 19 19 19 19 19 19 19 19 19 19		PLEELPRE	776	n a	A C	66.
PLENTAGE PURGVGLSPF PROGLE		PULMINACE BINDAGE	174	ာတ	. 6	9 2 2
PAYRPPNA 129 9 16 PPAYRPPNA 129 9 19 PPAYRPPNA 129 9 19 PPAYRPPNA 129 9 19 PPAYRPPNA 58 9 17 CLUPANDAL 8 9 11 RIVGLIGFA 624 9 19 SLUVSART 194 9 19 SLUVSART		PI PIHTAFI	711	<b>o</b>	9 -	08
PPAYRPPNA         129         9         19           PPHGGLIGW         58         9         17           QLDPABDAL         8         9         16           RLUPGSL         187         9         16           RLVADFSGF         376         9         19           RLVADFSGF         376         9         19           RLVADFSGF         357         9         20           RLVADFSAFY         416         9         19           SLDVSAAFY         416         9         16           SLDVSAAFY         416         9         16           SLDVSAAFY         416         9         16           SLDVSAAFY         416         9         16           SLDVSAAFY         150         1         9         16           SPANYTGGV         150         1         9         16           TPARYTGGY         16         9         16 <td></td> <td>PMGVGLSPF</td> <td>505</td> <td>6</td> <td>16</td> <td>08</td>		PMGVGLSPF	505	6	16	08
PPHGGLLGW 58 9 17 OLDPARDV. 8 9 17 RILTPOSL. 187 9 16 RILTPOSL. 187 9 16 RIVDESCH 376 9 19 RIVDESCH 357 9 20 SLDSWMTSL 194 9 19 SLDSWMTSL 194 9 19 SLDVSAFY 416 9 19 SLDVSAFY 416 9 19 SLDVSAFY 54 9 19 SLDVSAFY 54 9 19 SLDVSAFY 190 9 15 SVFFSWLSL 330 9 16 TWKAGILY 150 9 16 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 636 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119 TOCGYPALM 691 9 119		PPAYRPPNA	129	6	19	95
187 9 16 187 9 9 16 624 9 9 16 357 9 9 18 357 9 9 19 416 9 9 19 337 9 9 19 350 9 16 190 9 16 150 1 9 9 16 15 9 16 15 9 16 15 15 9 19 16 9 19 17 9 9 19 18 13 9 9 19 18 19 18 19 1		PPHGGLLGW	28	6	17	85
187 624 9 376 9 194 416 9 416 9 581 9 581 9 15 16 19 16 19 16 19 16 19 16 19 16 19 10 11 11 12 13 14 15 16 17 18 19 19 19 19 19 19 19 19 19 19		OLDPARDVL	<b>ω</b> .	<b>o</b>	16	80
376 9 9 18 357 9 9 19 194 9 9 19 416 9 9 19 337 9 9 19 581 9 9 19 150 • 9 16 150 • 9 16 150 • 9 16 150 • 9 16 150 9 9 16 150 150 9 9 16 150 9 9 16 150 9 9 16 150 9 9 16 150 9 9 17 150 9 9 17 150 9 9 19 160 9 9 19 17 180 9 9 19 180 9 9 19 180 9 9 19 180 9 9 19 180 9 9 19 180 9 9 19 180 9 9 19 180 9 9 19 180 9 9 19 180 9 9 19 180 9 9 19 180 9 9 19		. RILTIPOSL	187	6	16	80
357 9 9 19 194 9 9 19 416 9 9 19 337 9 9 19 581 9 9 15 330 9 16 150 • 9 16 150 • 9 16 150 • 9 16 150 10 150 10 150 10 150 10 170 10 180 10 180 10 190		RIVGLLGFA	624	<b>න</b> (	æ ;	06
194 9 9 19 416 9 9 19 581 9 20 581 9 9 19 350 9 16 190 9 16 150 9 16 636 9 9 15 15 9 19 15 19 17 92 18 19		RLWDFSOF	3/6	<b>.</b>	90	o 6
194 416 337 581 581 581 581 581 581 582 583 583 584 583 584 583 584 583 584 583 584 583 584 584 584 584 584 584 584 584		RVTGGVRLV	35/	<b>.</b>	70	001
337 9 9 19 581 9 9 15 350 9 15 330 9 16 150 • 9 18 631 9 18 16 9 19 17 15 18 19 19 19 19 19 19 19		SLDSWWTSL	46.	<b>.</b>	э ( - т	ກເ
SLIVEYOUN 581 9 15 15 15 15 15 15 15 15 15 15 15 15 15		SLDVSAAFY	337	no	6 C	82 101
SLRGLPVCA 54 9 19 SLRGLPVCA 350 9 15 SVRFSMLSL 330 9 9 16 TPQSLDSW 190 9 18 TPARVTGCV 354 9 18 TPGCYPALM 691 9 119 TVQASKLCL 16 9 115 TVWLSVIWM 352 9 115 VLCLRPVGA 133 9 17 VLDYGGML 259 9 17 VLDYGGML 259 9 17		SINEMGYVI	581	<b>.</b>	2 -	75
SPTWLSVI     350     9     15       SVRFSMLSL     330     9     16       TPQSLDSW     190     9     18       TPMKGILY     150     9     18       TPARVTGCV     354     9     18       TPGCYPALM     691     9     15       TVQASKLCL     16     9     16       TVMLSVINM     352     9     15       VLCLRPVGA     13     9     18       VLCLRPVGA     13     9     16       VLDYGGML     259     9     17       VLDYGGML     259     9     17		SI BGI PVCA	54	6	. 61	96
SVAFSMLSL       330       9       16         TIPQSLDSW       190       9       18         TLWKAGILY       150       •       9       18         TPABVTGGV       354       9       18         TPGCYPALM       691       9       15         TVQASKLCL       16       9       16         TVMLSVINM       352       9       16         VLCLRPVGA       15       9       16         VLCLRPVGA       133       9       18         VLDYGGML       259       9       17         VLDYGGML       259       9       17		SPTVWLSVI	350	6	15	7.5
THOSLDSW 190 9 18  TLWKAGILY 150 • 9 20  TLWKAGILY 354 9 20  TPARVTGGV 354 9 18  TOCGYPALM 636 9 19  TVQASKLCL 16 9 15  TVCLRPVGA 15 9 15  VLCLRPVGA 15 9 15  VLCLRPVGA 15 9 18  VLDYGGKHAL 92 9 17  VLDYGGKL 133 9 17  VLDYGGKL 259 9 17		SVRFSWLSL	330	6	16	80
TLWKAGILY 150 1. 9 20 TPARVTGGV 354 9 9 18 TPGWGLAI 691 9 15 TQCGYPALM 636 9 1 15 TVQASKLCL 16 9 15 TVMLSVIWM 352 9 15 VLCLRPVGA 15 9 15 VLCLRPVGA 13 9 18 VLDYGGKL4C 92 9 17 VLDYGGKL 259 9 17		TIPOSLDSW	190	6	18	06
TPARVTGGV         354         9         18           TPGWGLAI         691         9         15           TQCGYPALM         636         9         19           TVQASKLCL         16         9         16           TVMLSVIWM         352         9         16           VLCLRPVGA         15         9         18           VLGCRP4C         133         9         18           VLHKRILGL         92         9         17           VLDYGGML         259         9         17		TLWKAGILY	150	თ	20	100
TPTGWGLAI         691         9         15           TQCGYPALM         636         9         19           TVQASKLCL         16         9         19           TVMLSVIWM         352         9         15           VLCLRPVGA         15         9         19           VLGCRP4Q         133         9         18           VLHKRTLGL         92         9         17           VLDYGGML         259         9         17		TPARVTGGV	354	6	18	06
TOCGYPALM         636         9         19           TVQASKLCL         16         9         16           TVMLSVIWM         352         9         15           VLCLRPVGA         15         9         19           VLGCRH-QL         133         9         18           VLHKRTLGL         92         9         17           VLDYGGML         259         9         17		TPTGWGLAI	691	<b>o</b>	15	7.5
TVQASKLCL         16         9         16           TVWLSVIWM         352         9         15           VLCLRPVGA         15         9         19           VLGGCRH-VL         133         9         18           VLHKRTLGL         92         9         17           VLDYGGML         259         9         19		TOCGYPALM	989	6	19	95
TVWLSVIWM 352 9 15 VLCLRPVGA 15 9 19 VLGGCRH4Q 133 9 18 VLHKRTLGL 92 9 17 VLDYGGML 259 9 19		TVQASKLCL	16	6	16	80
VLCLRPVGA         15         9         19           VLGGCRH4Q         133         9         18           VLHKRTLGL         92         9         17           VLDYGGML         259         9         19		TVWLSVIWM	352	G	15	7.5
133 9 18 92 9 17 259 9 19		VLCLRPVGA	15	o	19	92
92 9 17 259 9 19		<b>M.GGCRHAL</b>	133	<b>o</b>	18	06
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		VLHKRTLGL	92	<b>o</b> n (	17	82
		VLLDYOGML	259	<b>D</b>	5	4

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ncy SEQ ID NO:	1800	1801	1802	1803	1804	1805	1806	1807	1808	1809	1810	1811	1812	1813	1814	1815	1816	1817	1818	1819	1820	1821	1822	1823	1824	1825	1826	1827	1828	1829	1830	1831	1832	1833	1834	1835	1836	1837	1838	1839		1840	1840 1841	1840 1841 1842	1840 1841 1842 1843	1840 1841 1842 1843 1844
Conservancy (%)	85	80	80	98	100	96	95	06	06	95	75	06	95	. 95	95	100	06	82	7.5	80	85	06	82	95	95	80	80	80	7.5	95	85	96	95	06	92	95	7.5	85	06	95		95	95 80	9 8 9 8 0 8 8 0 8	95 80 95 75	9 8 9 8 9 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9
Sequence Frequency	17	16	16	. 19	20	19	19	18	18	19	15	. 42	19	19	19	20	18	17	15	16	17	18	17	19	19	16	16	16	15	6-	17	19	. 61	18	19	19	15	17	18	19		19	19	19 16 19	61 9 1 6 1 5 1	91 91 92 72 71
No. of Amino Acids	6	o	6	თ	o	o	o	o	<b>o</b> .	<b>.</b>	6	<b>o</b>	10	10	10	10	10	10	10	10	10	10	10	10	10	10	. 10	10	10	10	10	10	10	10	10	10	10	10	10	10	Ç	2	5 0	5 0 0	2000	2000
Position	741	759	751	414	335	237	393	118	538	. 640	ĸ	768	521	633	516	312	533	23	239	7	622	31	59	14	43	243	248	246	171	513	4-	530	346	132	57	509	348	29	49	19	173	2	507	507 123	507 123 569	507 123 569 429
Sequence	VLSRKYTSF	WILRGTSFV	WLLGCAANW	WLSLDVSAA	WLSLLVPFV	WMCLRRFII	WPKFAVPNL	YLVSFGVWI	YMDDVVLGA	YPALMPLYA	YOHFBIGILL	YVPSALNPA	AICSVVRRAF	APFTQCGYPA	AQFTSAICSV	CIPIPSSWAF	CLAFSYMDDV	CLGWLWGMDI	CLRAFIIFLE	COLDPARDVL	CORINGLLGF	DIDPYKEFGA	DLLDTASALY	DVLCLRPVGA	· ELLSFLPSDF	FIIFLFILL	FILLCLIFL	FLFILLCU	FLGPLLVLOA	FLLAQFTSAI	FPDHOLDPAF	FPHCLAFSYM	FVGLSPTVWL	FALGGCRHAL	GLPVCAFSSA	GLSPFILAQF	GLSPTVWLSV	GMDIDPYKEF	GPCALRFTSA	GPLEEELPRL	1000 M1 200	しらとつしょうしら	GVGLSPFLLA	GVGLSPFLA GVWIRTPPAY	GVGLSPFLA GVWIRTPPAY HLNPNKTKRW	GVGLSPFLA GVGLSPFLA GVWIRTPPAY HLNPNKTKRW HPAAMPHLLV
Protein	ă	젙	ಶ	절	BN Na	<b>8</b> 6	점	SI SI	절	절	젒	절	젍	절	절	<b>8</b> 6	젙	3	<b>№</b>	×	절	2	2	×	2	₩	<b>}</b>	<b>№</b>	<b>₩</b>	ಕ	AN M	್ಷ	<b>8</b>	×	×	전	<b>№</b>	27	×	절		<b>§</b>	≩ &	≩	를 적 <del>경</del> 절	를 적 <del>것</del> 절 절

Sequence         Position         No. ol         Sequence         Consistion Annino Adds         Frequency         (%)           LLLCLFLL         249         10         20         100           LLLCLFLL         249         10         10         100           ILMCRISHY         313         10         16         80           IPMTACGARTAGA         21         10         10         10           IPMTACGARTAGA         23         10         16         80           IPMTACGARTAGA         23         10         16         80           ILMCHISTORY         610         10         16         80           ILMCHASHIGL         31         10         16         80           ILMLORGAMINA         489         10         17         85           ILMLORGAMINA         251         10         17         85           ILMLORGAMINA         252         10         10         10           ILLOHALIA         253         10         10         10           ILLOHALIA         254         10         11         85           ILLOHALIA         254         10         10         10           ILLOHALIA	Sequence         Position         No. old         Sequences         Conseivancy         (%)           LLLCLIFLL         249         10         20         100           LLLCLIFLL         249         10         20         100           LLLCLIFLY         139         10         20         100           ILMSTERETY         139         10         20         100           ILMSTERETY         139         10         16         80           IRMSTERM         21         10         16         80           IRMSTERM         23         10         16         80           IRMSTERM         23         10         16         80           IRMSTERM         23         10         16         80           IRMSTERM         234         10         16         80           IRLOCANMIL         234         10         16         80           ILLOCANMIL         234         10         16         80           LUCHALM         250         10         10         10           LUCHALM         252         10         10         10           LUCHALM         253         10         10	Table XIV		HBV B63	HBV B62 Super Motif			
LILCUFIL   249   10   20   10   10   10   10   10   10	LICUTCHEL	Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO
Light Name	Light Staylor   16   16   16   16   16   16   16   1	8	ILLICLIFIL	249	10	20	100	1847
HERENAMEN   133   10   10   10   10   10   10   1	Light National Color	<u>ಕ</u>	ILRGTSFVYV	092	0 :	16	80	1848
PHYCOCKSPK	PHINOGRAPH	<b>S</b>	ILSTLPETTV	139	20	20	100	1849
MANTHACAST   50   10   10   10   10   10   10   10	MATHEMATE   10   10   10   10   10   10   10   1	£ 6	IPIPSSWAFA	313	2	9 7	0 0	1850
KLAL'SHAIN	KUZGANIWGAH         21         10         17         86           KUZGANIWGAH         489         10         17         86           KUZHISHPIT         613         10         17         86           KOAFITSPY         653         10         17         86           KOAFITSPY         653         10         17         86           KOAFITSPY         653         10         17         86           MCDAMILL         254         10         17         86           LICLCHILL         254         10         17         86           LICLCHILL         256         10         17         86           LICLCHILL         256         10         16         90           LILCCHANAL         256         10         16         90           LILLCHILL         256         10         16         90           LILLCHILL         256         10         10         10	d 2	IPMGVGLOPF	20	2 0	20	100	1852
KULYSHPI  489   10   16   80	KUH,VSFPII         618         10         16         80           KOAPIREPIOW         610         10         16         80           KOAPIREPIOM         610         10         17         85           KOLARERIGIL         91         10         17         85           KOLARERIGIL         91         10         17         85           KOLARERIGIL         91         10         17         85           KOLARERIGIL         254         10         17         85           LULICASAMINI         252         10         16         90           LLICASAMINI         252         10         16         90           LLICASAMINI         252         10         16         90           LINDOGAM         257         10         16         90           LINDOGAM         252         10         10         90           LINDOGAM         253         10         10         10	2	KICKEM	21	2	17	85	1853
KAPANGPIDM         610         10         16         80           KOAFTSPTY         655         10         17         85           KNOCAFTSPTY         655         10         17         85           KNOCAPITALIA         254         10         17         85           LICHALIA         254         10         18         95           LICCHALIA         256         10         16         10           LICCHALIA         256         10         16         80           LICCHALIA         256         10         16         80           LICCHALIA         256         10         16         80           LICCHALIA         256         10         10         10           LILLOHALIA         257         10         10         95           LINDAGRA         175         10         19         95           LINDAGRA         172         10         10         10           LINDAGRA         173         10         10         10           LINDAGRAM         173         10         11         10           LINDAGRAM         17         10         10         10	KOAFMENDA         610         10         16         80           KOAFMENDA         653         10         19         95           KNOGAMETERY         653         10         17         85           KNOGAMETERY         254         10         17         85           LICHELLA         256         10         16         95           LIDCAMMIL         256         10         16         95           LIDCAMMIL         256         10         16         95           LICUFILLA         256         10         16         95           LICUFILLA         256         10         16         95           LICUFILLA         256         10         16         95           LILOMOGER         257         10         19         95           LILLADOGAM         257         10         19         95           LILLADOGAM         257         10         16         95           LILLADOGAM         257         10         16         95           LILLADOGAM         258         10         16         95           LILLADOGAM         258         10         16         16	절	KLHLYSHPII	489	10	16	80	1854
KOAPTRSPY         653         10         15         95           KOCAPTRSPY         653         10         17         85           KOLAFRESTY         653         10         17         85           LICLIFILIUM         254         10         17         85           LICCIPILIA         254         10         18         90           LICCIPILIA         256         10         16         80           LICCIPILIA         256         10         16         80           LICOHAMI         256         10         10         10           LILOURIUM         256         10         10         10           LILOURIUM         257         10         18         95           LILOURIUM         257         10         18         95           LIVIDOGRAM         257         10         18         95           LIVIDOGRAM         258         10         17         85           LIVIDOGRAM         258         10         17         85           LIVIDOGRAM         258         10         15         95           LIVIDOGRAM         258         10         15         10	KOCAPITESPY         653         10         15         95           KOCAPITESPY         653         10         17         85           KULMGRIGIL         31         10         17         85           LICLIPLUO         254         10         17         85           LICLIPLUO         254         10         17         85           LICLIPLUO         256         10         16         95           LICLIPLUO         256         10         16         80           LICCAMANIL         256         10         16         80           LICLIPLUO         257         10         16         80           LICCAMANIL         256         10         16         80           LICCAMANIL         257         10         16         80           LICCAMANIL         256         10         16         80           LICCAMANIL         257         10         16         80           LICCAMANIL         258         10         16         80           LICCAMANIL         257         10         16         80           LICCAMANIL         375         10         10         10	젒	KLPVNRPIDW	610	. 01	16	089	1855
KNOCHWOLL         620         10         17         85           KNOCHWOLL         254         10         17         85           LULVLLV         254         10         17         85           LLDYCAMP         256         10         16         95           LLDYCAMP         256         10         16         95           LLGCAAWH         722         10         16         95           LLGCAAWH         725         10         16         95           LLGCAAWH         725         10         16         95           LLALDAGEH         73         10         19         95           LLALDAGEH         775         10         19         95           LLALDAGEH         772         10         19         95           LLALDAGEH         75         10         17         85           LLALDAGEH         15         10         17         85           R	KNADSHIGLIL         610         17         85           KNADSHIGLIL         610         17         85           LILLUFLUT         254         10         17         85           LILLOFILLY         256         10         19         95           LILLOFILLY         256         10         16         95           LILLOFILLY         256         10         16         95           LILLOFILLY         256         10         20         100           LILLOFILLY         256         10         20         100           LILLOFILLY         256         10         20         100           LILLOFICHA         378         10         20         100           LILLOFICHA         378         10         18         95           LILLOFICHA         37         10         10         10           LILLOFICHA<	절	KOAFTFSPTY	653	10	19	. 56	1856
NUMERITICAL   91   10   17   85	WILHARTIGL         91         10         17         85           UICHALIN         254         10         19         95           UICHALIN         254         10         19         95           ULCGAMIN         752         10         10         10           ULCCAMIN         752         10         10         10           ULGCAMIN         752         10         10         10           ULGCAMIN         752         10         10         10           ULPFCOLINY         378         10         19         95           LIALOAGER         772         10         10         10           LIALOAGER         772         10         10         10           LIALOAGER         773         10         10         10           LIALOAGER         75         10         10         10           ALSINGARMA         75         10         10         10           <	ಶ	KVCQRIVGIL	620	9 :	17	85	1857
LICHCHUND         254         10         95           LICHCLULU         254         10         10         95           LICCARAWI         752         10         16         90           LICATAGAR         44         10         20         100           LISTAGORF         44         10         19         95           LIVIADAGAR         772         10         18         95           LIVIADAGAR         772         10         18         95           LIVIADAGAR         772         10         16         86           LIVIADAGAR         772         10         16         86           LIVIADAGAR         75         10         16         86           LIVIADAGAR         75         10         16         86           LIVIADAGAR         75         10         10         10           NISIPINALOM         75         10         10         10           NISPINA	ILCLIPLUX	×	KYLHKRTLGL	91	0 :	17	85	1858
LICOLILLY	LICCAMANILLY	<b>8</b>	LIFLLVLLDY	254	10	19	95	1859
LILDYGAMWIN  LILDY	LIDYGAMINAY   250   10   16   910   11   11   12   910   11   12   910   12   910	<b>≥</b> 26	LICUFLEN	251	0 ;	50	100	1860
LLCSANWANTL LLCSANWANTL LLCSANWANTL LLCSANWANTL LLCSANWANTL LLSPECIM LLMLDYGGR LLMLONGSR LLMMWANGSR LLMLON	LICOLHELIA   250   100	<b>}</b>	LDYGGMLPV	092	5 5		0 0	1861
LINGGRAM   178   10   20   100   1	LUMPICOMM 378 10 20 100 11 100	₫ 2	LEGCAANWIL	250		0-0	100	1863
LISRIPSOFF 44 10 19 95 LUALDYCSM 257 10 19 95 LUALDYCSM 257 10 19 95 LUALDYCSM 257 10 19 95 LUALDYCSM 257 10 19 95 LUALDYCSM 338 10 19 95 LUALDYCSM 338 10 19 95 LUALDYCSM 89 10 10 19 95 LUALDYCSM 123 10 10 10 10 10 10 10 10 10 10 10 10 10	LISFLPSDFF         44         10         19         95           LLLUDYCAM         257         10         19         95           LLLUDYCAM         338         10         19         95           LLYLDYCAMPY         338         10         19         95           LLYLDAGMAY         338         10         17         89           LINLDYGAMY         258         10         17         80           LINLDYGAMY         258         10         17         80           LINLDYGAMY         258         10         16         80           LINLDYGAMY         258         10         17         80           LINLDYGAMY         258         10         16         80           LINLDYGAMY         258         10         17         85           NASPANAMY         406         10         18         90           NASPANAMY         47         10         16         17         85           NASPANAMY         47         10         10         10         10           PHYARAMY         42         10         10         10         10           PLDFCAMY         42         10	; <u>≥</u>	II PIFFCI WV	378	10	50	100	1864
LIVLDYGGM 257 10 19 95  LLVLDYGGFL 338 10 19 95  LLVPPCUMYN 379 10 20 100  LPHTAELLA 712 10 17 85  LPLDKGIFPL 123 10 20 100  LPLDKGIFPL 123 10 20 100  LVLDYGGFL 176 10 19 95  LVLDYGGFL 176 10 19 95  LVLDAGFFL 178 10 10 19 95  LVLDAGFFL 178 10 10 19 95  LVLDAGFFL 178 10 10 17 85  NLSVPNPLGF 57 10 10 18 90  NLSVPNPLGF 57 10 10 17 85  NRVKTRAWGGY 47 10 20 100  PLEELPALA 7713 10 10 20 100  PLEELPALA 7713 10 10 20 100  PLEELPALA 174 10 20 10 100  PLEELPALA 174 10 20 10 100  PLEELPALA 174 10 10 20 100  PLEELPALA 177 10 10 10 100  PLEELPALA 177 10 10 10	LIVLDOYGGM 257 10 19 95 LLVLDOYGFH 175 10 19 95 LLVLDOGFFL 338 10 19 95 LLVPPCOGFF 338 10 19 95 LLVPPCOGFF 338 10 19 95 LPIFTCLWYY 379 10 20 100 LPIFTCLWYY 379 10 20 100 LPIFTCLWYY 123 10 10 16 86 LVLLDOGGIRPY 123 10 20 100 LVLLDOGGIRPY 123 10 10 19 95 LVLLDOGGIRPY 124 10 10 15 15 100 LVLLDOGGIRPY 124 10 10 100 LVLLDOGGIRPY 124 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 10 100 LVLLDOGGIRPY 124 10 10 100 LVLLDOGGIRPY 124 10 10 100 LVLLDOGGIRPY 124 11 10 10 100 LVLLDOGGIRPY 124 11 10 10 100 LVLLDOGGIRPY 124 11 10 10 100 LVLLDOGGIRPY 124 11 10 10 100 LVLLDOGGIRPY 124 11 10 10 100 LVLLDOGGIRPY 124 11 10 10 100 LVLLDOGGIRPY 124 11 10 10 100 LVLLDOGGIRPY 124 11 10 10 100 LVLLDOGGIRPY 124 11 10 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 10 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLDOGGIRPY 124 11 100 LVLLD	2	LISFLYSDFF	4 4	10	- 6-	95	1865
LIMOAGFR         175         10         18         90           LUNDAGFR         175         10         19         95           LUFPCLWNY         379         10         20         100           LPHTAELLA         712         10         20         100           LPLOKGIRPY         123         10         20         100           LPLOKGIRPY         258         10         19         95           LVLDYGGML         258         10         19         95           LVLDYGGFL         176         10         19         95           LVLDYGGML         258         10         10         18         90           LVLDYGGML         156         10         10         18         90           NLSVINAN         406         10         17         85           NLSVINAN         57         10         15         75           NLSVINANCORI         616         10         17         85           PHTACLWAY         57         10         10         10           PHTACLWAY         71         10         20         100           PHTACHARA         71         10         20	LIVLOAGFR         175         10         18         90           LIVLOAGFR         175         10         19         95           LIVLOVACHALLA         712         10         20         100           LIVLOAGFLLA         712         10         20         100           LIVLOAGFLLA         123         10         20         100           LIVLOAGFLLA         176         10         19         95           LIVLOAGFLLA         178         10         19         95           LIVLOAGFLLA         176         10         19         95           NILSSMISM         406         10         18         90           NILSSMISM         47         10         15         75           NINSWINGSIN         571         10         15         75           NINSWINGSIN         47         10         17         85           PIEFCLWYI         47         10         10         10	NB NB	LVLDYOGM	257	10	19	95	1866
LUMPHOWNY         338         10         19         95           LUMPHOWNY         379         10         20         100           LPLDKGIKPY         123         10         17         86           LPLDKGIKPY         123         10         16         80           LPLDKGIKPY         258         10         16         80           LVLDYGGHL         258         10         18         90           LVLDYGGFLL         15         10         18         90           NLSSNLSM         406         10         18         90           NLSSNLSM         47         10         18         90           NLSSNLSM         47         10         15         75           NWSIPWTHKY         47         10         17         85           PIDKGIKPYY         124         10         17         85           PLIPRAMPHH         427         10         20         100	LUMPCOMINA         338         10         19         95           LUMPACUMY         712         10         17         85           LPHTAELLA         712         10         17         85           LPMALMRTA         89         10         16         80           LPMALSTRAM         258         10         19         95           LVLDYGGML         176         10         19         95           NASPWARSAM         360         10         17         85           NASPWARSAMAMAK         47         10         15         75           NASPWARSAMAM         20         10         10         10         10           PLIFELPHA         20         10         10         10         10           PLIFELDAL         10         10         10         10         10           PLIFFELDAL         10         10         10         10         10           PLIPARAMPH         427<	<b>&amp;</b>	LLVLOAGFFL	175	10	18	06	1867
PHPFCLWWY	LIPPCALWAY         37.9         10.0         17.0         10.0           LIPPCALWAY         71.2         10.0         17.0         10.0           LIPPCALMARTIL         89         10         12.0         10.0           LIPPCALMERTL         12.3         10         1.0         10.0         10.0           LINDYGAFLL         17.6         10         1.0         10.0 <td><u>~</u> :</td> <td>LLVPFVQWFV</td> <td>338</td> <td><u> </u></td> <td>6-0</td> <td>95</td> <td>1868</td>	<u>~</u> :	LLVPFVQWFV	338	<u> </u>	6-0	95	1868
LYNLHKRTL         89         10         16         80           LVLDYGGMY         123         10         16         80           LVLDYGGMY         123         10         19         95           LVLDYGGMY         176         10         18         90           MAWAYAGFEL         176         10         18         90           MAWAYAGFEL         15         10         17         85           NLSSNLSM         406         10         17         85           NLSSNLSM         406         10         17         85           NLSSNLSM         406         10         17         85           NSPAPINGF         15         10         15         75           NSPAPINGF         57         10         15         75           NVSIPWTHKWWY         47         10         17         85           PIFFCLWYI         380         10         17         85           PLHAAMPH         47         10         10         10           PLHPAAMPH         427         10         10         10           PLHPAAMPH         427         10         10         10	LPKOLHKRTL         89         10         16         80           LPLDKGIKPY         123         10         16         80           LVLDAGGIKPY         123         10         19         95           LVLDAGFELL         176         10         18         90           MAWWYNGPSLY         360         10         17         85           NLSSNLSML         406         10         17         85           NUSPWTHACY         47         10         20         100           PIDMCKONNY         380         10         17         85           PLDKGIKRYY         124         10         17         85           PLDKGIKRYY         124         10         20         100           PLDRGIKRYY         124         10         19         95           PLDKGIKRYY         124         10         10         10	<u> </u>	I PIHTAELLA	712	9 0	17	85	1870
LPLDKGIKPY         123         10         20         100           LVLDYGGML         258         10         19         95           LVLDYGGML         176         10         18         95           LVLDYGGML         360         10         17         85           MAMAWYGSLY         360         10         17         85           NLSSNLSWL         406         10         18         90           NLSSNLSWL         406         10         17         85           NPWTRGWGY         571         10         15         75           NPWTRGWGY         571         10         15         75           NPWTRGWGY         571         10         17         85           PILYACLAA         713         10         17         85           PLKGFFDHAL         10         10         17         85           PLHPAAMPHL         427         10         10         10           PLPIFCLW         10         10         10         10           PLHPAAMPHL         427         10         10         10           PLINLOGGFF         174         10         16         80	LPLDKGIKPY         123         10         20         100           LVLDXGGRAL         258         10         19         95           LVLDXGGFL         176         10         18         90           MAMWYWGPSLY         360         10         17         85           NLSSNLSML         406         10         18         90           NLSSNLSML         406         10         18         90           NLSSNLSML         47         10         15         75           NLSSNLSML         47         10         15         75           NPINCKRWGY         571         10         15         75           NPINCKRWGY         571         10         17         85           PIHTAELLAA         713         10         17         85           PLHGKIRPY         124         10         17         85           PLHFALLAA         124         10         10         10           PLHFALMPAL         427         10         10         10           PLHFALMPAL         427         10         10         10           PLHFALL         174         10         10         10 <t< td=""><td>×</td><td>· LPKVLHKBTL</td><td>68</td><td>10</td><td>16</td><td>08</td><td>1871</td></t<>	×	· LPKVLHKBTL	68	10	16	08	1871
LVLDYOGAML 258 10 19 95  LVLDYOGAML 258 10 19 95  LVLDYOGAML 176 10 18 90  MAWWYWGPSLY 406 10 17 85  NLSSNLSWL  NLSSNLSWL  A 15 10 15 75  NPANTARWSY 47 10 10 17 85  NVSIPWTHKY 47 10 10 17 85  NVSIPWTHKY 124 10 10 20 100  PLIPTECLAM 124 10 10 19 95  PLUPTECLY  PLUPAMPHL 427 10 10 20 100  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUPTECLY  PLUCAGFF  PLUPTECLY	LVLDYOGML         258         10         19         95           LVLOAGFFLL         176         10         18         95           NAMYWYGPSLY         406         10         17         85           NLSNPNPLGF         15         10         18         90           NLSNPNPLGF         571         10         15         75           NPINTARLAG         571         10         15         75           NVSIPWTHKY         47         10         20         100           PINTAELLAA         713         10         20         100           PINTAELLAA         713         10         20         100           PLIKGIKPYY         124         1         1         10         20         100           PLIKGIKPYY         10         10         10         10         10         10           PLIKGIKPYY         10         10         10         10 </td <td>ಕ</td> <td>LPLDKGIKPY</td> <td>123</td> <td>10</td> <td>20</td> <td>100</td> <td>1872</td>	ಕ	LPLDKGIKPY	123	10	20	100	1872
LVLOAGFFLL 176 10 18 90  MAWWWGPSLY 360 10 17 85  NLLSSNLSML  NLLSSNLSML  15 10 18 90  NLLSSNLSML  15 10 18 90  NLLSSNLSML  15 10 15 75  NVSIPWTHKY  47 10 20 100  PIFFCLWYI 380 10 20 100  PIFFCLWYI 380 10 17 85  PLDKGIKPYY 124 10 10 20 100  PLDKGIKPYY 124 10 10 19 95  PLUPAAMPHL 427 10 20 100  PLUNLOAGFF 174 10 10 19 95  PLUNLOAGFF 174 10 10 16 80  PLINLOAGFF 20 10 100  PLINLOAGFF 174 10 10 16 80  PLINLOAGFF 20 10 100  PLINLOAGFF 20 10 100  PLINLOAGFF 377 10 10 16 80  PLINLOAGFF 377 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 16 80  PLINLOAGFF 371 10 10 10 10 10 10 10 10 10 10 10 10 10	LVLOAGFPL 176 10 18 90  MMWWWGPSLY 360 10 17 85  NLLSSNLSML  NLSSNLSML  15 10 18 90  NLSSNLSML  47 10 15 75  NPMKTRGWGN  NVSIPWTHKV  47 10 20 100  PIFFCLWWYI  PILPIFFCLWYI  PLEELPRIA 20 10 10 18 90  PLEELPRIA 10 10 18 90  PLIPIFFCLW  PLAAAMPHL 427 10 10 19 95  PLIPIFFCLW  PLINIAGELEA 377 10 10 19 95  PLIPIFFCLW  PLINIAGELEA 377 10 10 19 95  PLIPIFFCLW  PLINIAGELEA 377 10 10 16 80  PLIPIFFCLW  PLINIAGELEA 377 10 10 16 80  PLIPIFFCLW  PLINIAGELEA 377 10 10 16 80  PLIPIFFCLW  PLINIAGELEA 377 10 10 16 80  PLIPIFFCLW  PLINIAGELEA 377 10 10 16 80  PLIPIFFCLW  PLINIAGELEA 377 10 10 16 80  PLIPIFFCLW  PLIPIFFCLW  PLIPIFFCLW  PLIPIFFCLW  10 10 19 95  PLIPIFFCLW  PLIP	<b>₩</b>	LVLLDYQGML	258	10	19	95	1873
MANNYWGPSLY 360 10 17 85  NLSSNLSWL 406 10 18 90  NLSSNLSWL 15 10 18 90  NULSSNLSWL 15 10 18 90  NNSIPWTHRY 47 10 10 20 100  PIDNOWCOCH 616 10 10 20 100  PIFCLWY1 380 10 20 100  PLEELPRIA 713 10 10 20 100  PLEELPRIA 10 10 20 100  PLHTACLLA 713 10 10 20 100  PLHTACLLA 713 10 10 20 100  PLHTACLLA 174 10 10 20 100  PLHTACLLA 174 10 10 10 20 100  PLHTACLLA 377 10 10 20 100  PLHTACLLA 377 10 10 20 100  PLHTACLLA 377 10 10 20 100  PLHTACLLA 377 10 10 20 100  PLHTACLLA 377 10 10 10 10 10 100  PLHTACLLA 377 10 10 10 10 100  PLHTACLLA 377 10 10 10 10 100  PLHTACLLA 377 10 10 10 10 100  PLHTACLLA 377 10 10 10 10 100  PLHTACLLA 377 10 10 10 10 100  PLHTACLLA 377 10 10 10 10 100  PLHTACLLA 377 10 10 10 100  PLHTACLLA 377 10 10 10 100  PLHTACLLA 377 10 10 10 100  PLHTACLLA 377 10 10 10 100  PHTACLLA 377 10 10 100  PHTACLLA 377 10 10 100  PHTACLLA 377 10 10 100  PHTACLLA 377 10 10 100  PHTACLLA 377 10 10 100  PHTACLLA 377 10 10 100  PHTACLLA 377 10 10 100  PHTACLLA 377 100  PHTACLLA 377 10 100  PHTACLLA 377 10 100  PHTACLLA 377 10 100  PHTACLLA 377 10 100  PHTACLLA 377 1000  PHTACLLA 377 1000  PHTA	MANAWAGPSLY         360         10         17         85           NLLSSNLSML         406         10         18         90           NLLSSPLSML         406         10         18         90           NLLSVPLYICF         15         10         15         75           NVSIPWTHKY         47         10         20         100           PIDWAKCAMACY         380         10         20         100           PILTACLLAA         713         10         17         85           PLDKGIKPYY         124         10         20         100           PLDKGIKPYY         124         10         20         100           PLDKGIKPYY         124         10         20         100           PLDKGIKPYY         124         10         10         10           PLDKGIKPYY         10         10         10         10           PLUNLOAGFE         174         10         10         10	<b>M</b>	LVLOAGFFIL	176	10	18	06	1874
NLLSSNLSWL  NLSNLSWL  NLSNPNPLGF  NSNPNPLGF  NNSIPWTHKN  15  NNSIPWTHKN  17  NNSIPWTHKN  17  NNSIPWTHKN  18  NNSIPWTHKN  18  NNSIPWTHKN  18  NNSIPWTHKN  18  NNSIPWTHKN  18  NISPWCKCORII  10  NUSIPWTHKN  10	NLLSSNLSWL  NLLSSNLSWL  NLSSNLSWL  NLSSNLSWL  NISSNPATIGF  15  NONSMANCACINI  NOSIPWTHKV  47  NOSIPWTHKV  47  NOSIPWTHKV  47  NOSIPWTHKV  47  NOSIPWTHKV  124  NOSIPWTHKV  NOSIPWTHKV  124  NOSIPWTHKV  124  NOSIPWTHKKL  125  NOSIPWTHKKL  126  NOSIPWTHKKL  126  NOSIPWTHKKL  127  NOSIPWTHKKL  126  NOSIPWTHKKL  127  NOSIPWTHKKL  126  NOSIPWTHKKL  127  NOSIPWTHKKL  128  NOSIPWTHKKL  126  NOSIPWTHKKL  127  NOSIPWTHKKL  128  NOSIPWTHKKL  100  NOSIP	<b>8</b>	MMWYWGPSLY	360	10	17	85	1875
NLSVPNPLGF 15 10 15 75 NPNCTKRWGY 571 10 15 75 NPNCTKRWGY 571 10 10 10 10 10 10 10 10 10 10 10 10 10	NLSVPNPLGF 15 10 15 75 NVSIPWTKRWGY 571 10 15 75 NVSIPWTKRWGY 47 10 10 20 100 PINTAELLAA 713 10 20 100 PINTAELLAA 124 10 20 100 PLHPAAMPHL 427 10 20 100 PLUPIFFCLW 377 10 20 100 PLUNCAGFF 174 10 10 20 100 PLUNCAGFF 174 10 10 20 100 PLINTAELL 711 10 10 16 80 PLNNEKBRL 2 10 16 80 PLNNEKBRL 2 10 16 80 PNGVGLSPFL 505 10 10 16 80	젒	NITSSNESWL	406	0 :	18	06	1876
NPNKTKRWGY NPNKTKRWGY NVSIPWTHKV 47 NVSIPWTHKV 47 NUSIPWTKCORI 616 N10 NSIPWTKCORI 616 N10 NSIPWTKCORI 616 N10 NSIPWTKCORI 616 NSIPMTKCORI 616 NSIPMTKCORI 616 NSIPMTKCORI 616 NSIPMTKCORI 616 NSIPMTKCORI 616 NSIPMTKCORI 617 NSIPMTKCORI 618 NSIPMTKCORI 619 NSIPMTKCORI 619 NSIPMTKCORI 610	NPNKTKRWGY NVSIPWTHKV NVSIPWTHKV NSIPWTHKV NSIPWTHKV NSIPWTKCORI NSIPWTKCORI NSIPWTKCORI NSIPWTKCORI NSIPWTKCORI NSIPWTKCORI NSIPMTKCORI NSIPWTKCORI N	<b>8</b>	NLSVPNPLGF	15	<u> </u>	5.	75	1877
PUDWKVCQRI	NVSIPWI HKV         47         10         10         10           PIDWAVCQRI         616         10         17         85           PIFCLWYI         380         10         20         100           PIFTCLWYI         713         10         17         85           PLDKGIKPY         124         10         20         100           PLDKGIKPY         124         10         18         90           PLDKGIKPY         10         10         10         10           PLDKGIKPY         10         10         10         10           PLDKGIKPY         10         10         10         95           PLDKGIKPY         10         10         100         100           PLDKGIKPY         174         10         20         100           PLUALOAGF         174         10         20         100           PLYOMEKARI         2         10         10         10           PLYOMEKARI         98         10         15         85           PMGVGLSPR         10         10         10         10           PRAGAGLSPR         10         10         10         10	<b>₹</b> 8	NPNKTKRWGY	1/6	2 5	3.0	£ 5	18/8
PIFFCLWVI 380 10 20 100 PIFFCLWVI 380 10 20 100 PIFFCLWVI 124 • 10 17 85 PLDKGIKPYY 20 10 10 20 100 PLDKGIKPYY 20 10 10 19 95 PLHPAAMPH 427 10 20 100 PLUNCAGF 174 10 20 100 PLUNCAGF 174 10 10 85 PLINTAELL 711 10 16 80 PLINNEKARL 2 10 15 75 PLINNEKARL 98 10 10 10	PIFFCLWAYI         380         10         20         100           PIFFCLWAYI         380         10         20         100           PIHTALLAA         713         10         20         100           PLDKGIKPYY         124         •         10         20         100           PLDKGIKPYY         20         10         20         100           PLDKGIKPYY         10         10         10         95           PLAPAMPIA         427         10         20         100           PLUPIAMPHA         377         10         20         100           PLINIABELL         711         10         16         80           PLINIABELL         711         10         16         80           PLINIABELL         711         10         16         80           PLINIABELL         711         10         15         75           PRINIABELL         505         10         10         10           PRINIABELL         134         1         10         10           PRINIABELL         134         1         10         10           PRINIADELL         134         1         10	₹ 8	NOSIPWIHKV	616	2 5	7,	001 85	1880
PIHTACLIAN         713         10         17         85           PLDKGIKPYY         124         •         10         20         100           PLEELPRIA         20         10         18         90           PLAPAAMPHL         427         10         20         100           PLHPAAMPHL         427         10         20         100           PLUICAGFF         174         10         20         100           PLINIABELL         711         10         16         80           PLINIABELL         711         10         16         80           PLINIABELL         2         10         16         85           PLINIABELL         2         10         16         86           PLINIABELL         2         10         16         86           PLINIABELL         2         10         16         86           PLINIABELL         30         10         16         86	PIHTAELIA PUNCIRIPYY         713         10         17         85           PLDKGIKPYY         124         10         10         10         100	2 ≥	PIEGO WAY	380	2 2	20	100	1881
PLDKGIKPYY 124 • 10 20 100 PLDKGIKPYY 20 10 18 90 PLGFPDHOL 10 10 19 95 PLHPAAMPHL 427 10 20 100 PLUFCLW 377 10 20 100 PLUKLOAGFF 174 10 10 19 95 PLINTAELL 711 10 16 80 PLINNEKARL 2 10 15 75 PLINNEKARL 98 10 10 10	PLDKGIKPYY         124         •         10         20         100           PLDKGIKPYY         20         10         18         90           PLGFPDHOL         10         10         19         95           PLHPAAMPHL         427         10         20         100           PLUPIAMPHL         377         10         20         100           PLULOAGFF         174         10         19         95           PLINIABELL         711         10         16         80           PLINIABELL         2         10         15         75           PLINIABELL         2         10         15         75           PLINIABELL         34         10         16         86           PRINIABELL         134         10         10         100	ğ	PIHTAFILAA	713	10	17	85	1882
PLEELPRIA         20         10         18         90           PLHPAAMPHL         427         10         19         95           PLHPAAMPHL         427         10         20         100           PLHPAAMPHL         377         10         20         100           PLUNCAGFF         174         10         20         100           PLINTAELL         711         10         16         80           PLINTAELL         711         10         16         80           PLINTAERIL         98         10         16         80           PLINTAERIL         505         10         16         80	PLEELPRIA         20         10         18         90           PLGFPDHOL         10         10         19         95           PLHPAAMPHL         427         10         20         100           PLHPAAMPHL         377         10         20         100           PLUALCAGFF         174         10         20         100           PLINICAGFF         711         10         16         80           PLINICAGFF         2         10         16         80           PLINICAGESPR         2         10         15         75           PLINICAGESPR         98         10         17         85           PANGVGLSPR         505         10         16         80           PPINAPILST         134         1         10         16         80	절	PLDKGIKPYY	124	10	20	100	1883
PLGFFDHOL         10         19         95           PLHPAAMPHL         427         10         20         100           PLUPAAMPHL         377         10         20         100           PLUNCAGFF         174         10         19         95           PLINTAELL         711         10         16         80           PLYNEKRRL         2         10         15         75           PLYNEKRRL         98         10         16         80           PLYNEKRRL         505         10         16         80	PLGFFDHOL         10         19         95           PLHPAAMPHL         427         10         20         100           PLUPAAMPHL         377         10         20         100           PLUNCAGFF         174         10         19         95           PLINIABLL         711         10         16         80           PLINIBRAL         2         10         15         75           PLINIBRAL         98         10         17         85           PMGVGLSPRL         505         10         16         80           PPNAPILSTL         134         1         10         10	ಕ	PLEEELPRLA	20	10	18	06	1884
PLHPAAMPHL 427 10 20 100 PLUPIFFCLW 377 10 20 100 PLLVLOAGFF 174 10 19 95 PLINICAGEF 711 10 16 80 PLYNHEKARL 2 10 15 75 PLYNHEKARL 98 10 16 85 PLYNHEKARL 98 10 16 80	PLHPAAMPHL         427         10         20         100           PLUPIFFCLW         377         10         20         100           PLLVLOAGFF         174         10         19         95           PLLVLOAGFF         711         10         16         80           PLYOHERAR         2         10         15         75           PLYNEKARL         98         10         17         85           PMGVGLSPR         505         10         16         80           PPNAPILSTL         134         1         10         10	&	PLGFFPDHOL.	10	10	19	95	1885
PLLPIFFCLW         377         10         20         100           PLLNLOAGFF         174         10         19         95           PLPINTAELL         711         10         16         80           PLSYCHFRAL         2         10         15         75           PLYNEKARL         98         10         16         80           PROVINGESPPL         505         10         16         80	PLLVLOAGFF         377         10         20         100           PLLVLOAGFF         174         10         19         95           PLNITAELL         711         10         16         80           PLSYCHFRAL         2         10         15         75           PLYNEKARL         98         10         17         85           PMGVGLSPFL         505         10         16         80           PPNAPILSTL         134         1         10         100	젒	PLHPAAMPHL	427	10	20	100	1886
PLINLOAGFF 174 10 19 95 11 10 19 95 11 10 19 95 11 10 19 95 11 10 19 95 11 10 19 95 11 10 19 95 11 10 19 95 11 10	PLLVLOAGFF         174         10         19         95         1           PLPIHTAELL         711         10         16         80         1           PLSYCHFRIAL         2         10         15         75         1           PLYNEKRARL         98         10         17         85         1           PMGVGLSPR         505         10         16         80         1           PPNAPILSTL         134         1         10         100         1	<b>%</b>	PLLPIFFCLW	377	10	20	100	1887
PLYOHFAEL / 11 10 16 80 80 80 80 80 80 80 80 80 80 80 80 80	PLPIHTAELL     /11     10     16     80       PLSYOHFRAL     2     10     15     75       PLTNAEKRRL     98     10     17     85       PMGVGLSPFL     505     10     16     80       PPNAPILSTL     134     1     10     100	<b>8</b>	PLLVLOAGFF	174	0 9	6 9	95	1888
PLSYCHERKL 2 15 75 75 75 75 75 75 75 75 75 75 75 75 75	PLSYCHERKL 2 15 75 75 75 75 75 75 75 75 75 75 75 75 75	호 :	PLPIHTAELL	Ξ,	0 0	9 .	0 0 0	1889
PACINGLISH 505 10 16 80	PMGVGLSPFL 505 10 16 80 10 PPNAPILSTL 134 ; 10 20 100	로 8	PLSYCHFRKL	2 8 8	2 5		ر م م	1890
PARCIALISTIC CO. 10 00 00 00 00 00 00 00 00 00 00 00 00	PANGVGLSTL 134 ; 10 20 100	2 8	PLI VIVENSIAL	303		~ ¥	9 6	600
	PFNAPILSIL 134	₹ :	PMGVGLSPFL	700	<b>.</b>	9 6	000	1092

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SEQ ID NO:	1894	1895	1896	1897	1898	1899	1900	1901	1902	1903	1904	1905	1906	1907	1908	1909	1910	1911	1912	1913	1914	1915	1916	1917	1918	9191	1920	1921	1923	1924	1925	1926	1927	1928	1929	1930	1931	1932	1933	1934	1935	1936	1937	1938	1939	1940
Conservancy (%)	85	06	06	75	06	. 75	100	95	90	100	7.5	80	06	06	95	7.5	85	06	95	95	. 80	85	95	80	080	ი ი	C 4	n w	5 6	06	7.5	95	95	95	80	06	. 56	7.5	80	85	95	95	80	80	95	7.5
Sequence	17	18	18	15	18	15	20	19	18	20	15	16	18	18	19	15	17	18	19	19	16	17	19	16	9 ;	י ה ר	<u> </u>		20	8-	15	19	19	19	16	. 18	19	15	16	17	19	19	16	16	19	15
No. 01 Amino Acids	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	0 9	2 9	2 5	) C	2 -	0	10	=	=		gan i		_	=	<b>-</b>	- -	<del>-</del> '		-	<del></del>	-	
Position	612	66	624	106	56	818	337	54	403	49	350	330	. 190	354	128	22	543	133	340	398	17	740	525	759	751	4   4 9 C	756	359	147	263	2	633	516	397	312	533	253	239	14	622	40	φ	248	246	256	130
Sequence	PVNRPIDWKV	OLLWFHISC	RIVGLLGFAA	RLKLIMPARF	ROALCWGEL	RVHFASPLHV	SILVPFVOWF	SLRGLPVCAF	SLTNLLSSNL	SPHHTALROA	SPTVWLSVIW	SVRFSWLSLL	TIPOSLDSWW	TPARVTGGVF	TPPAYRPPNA	TPPHGGLLGW	VLGAKSVQHL	<b>M.GGCRHMLV</b>	VPFVQWFVGL	VPNLQSLTNL	VQASKLCLGW	WLSRKYTSF	WRRAFPHCI.	WILRGTSFVY	· WLLGCAANWI	WLSLDVSAAF	WLWGMDIDPY	WMANAMOBE	VI HTI WKAGI	YOGMLPVCPL	YOHFRALLL	APFTOCGYPAL	AQFTSAICSVV	AVPNLOSLTNL	CIPIPSSWAFA	CLAFSYMDDVV	CLIFLVLLDY	CLRRFIIFLFI	CPTVQASKLCL	CORIVGLLGFA	DLNLGNLNVSI	ELSPLSDFF	FILLCUFIL	FILLCIF	FLIVILDYOGM	FPAGGSSSGTV
Protein	Z	SE SE	전	젙	2	점	8	×	젍	STC STC	AG AG	<b>%</b>	EN.	<b>હ્</b>	2	SK BK	ಶ	×	&	젙	2	전 :	ರ	전 :	호 8	₹ 5	3 2	3 6	<u> </u>		절	젒	절	ಕ	<u>~</u>	쥖 :	26	<b>8</b>	ST.	ದ್ದ	전 :	2	<b>№</b>	NA NA	26	BN

SEQ ID NO:	1941	1942	1943	1944	1945	1946	1947	1948	1949	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	
Conservancy (%)	75	06	. 06	75	06	98	85	90	·80	80	100	100	06	80	06	80	80	100	7.5	100	100	06	95	06	85	100	85	100	80	80	98	80	75	95	06	06	92	82	80	100	100	100	06	80	7.5	80	9.2	
Sequence Frequency	15	18	18	15	18	19	17	18	16	16	20	20	18	16	18	16	16	20	15	20	20	18	19	18	17	20	17	20	16	16	19	16	15	19	18	18	19	1.7	16	20	20	20	18	16	15	16	19	
No. of Amino Acids	11		=		=	=	-1		Ξ	=	1	Ξ		=	=	Ξ	Ξ			=	=	=	=	-1-			=	<u> </u>	Ξ	=	=	11		· •		-11	11		=	=			11	11	11	=	11	
Position	749	132	992	348	19	173	. 26	. 52	491	244	249	139	188	504	625	503	489	251	63	250	378	407	257	175	100	379	712	123	611	178	339	433	-	42	411	774	<b>-</b>	616	496	138	427	377	174	711	2	505	129	•••
Sequence	FPWLLGCAANW	FALGGCRHALV	FVYVPSALNPA	GLSPTVWLSVI	GPLEEBLPRLA	GPLLVLOAGFF	GPLTVNEKRAL	HLSLRGLPVCA	HLYSHPIILGF	IIFLFILLICL	ILLICUFLLY	ILSTLPETTVV	ILTIPOSLDSW	IPMGVGLSPFL	IVGLLGFAAPF	KIPMGVGLSPF	KLHLYSHPIIL	LCLIFLY	LEWSPOADGI	LLICLIFLIAL	LLPIFFCLWVY	LLSSNLSWLSL	LLVLLDYOGML	LYLOAGFFLL	LLWFHISCLTF	LPIFFCLWVYI	LPIHTAELLAA	LPLDKGIKPYY	LPVNRPIDWKV	LOAGFFLLTRI	LVPFVQWFVGL	MPHLLVGSSGL	MPLSYQHFRKL	NLGNLNVSIPW	NLSWLSLDVSA	NPADDPSRGRL	NPLGFFPDHOL	PIDWKVCQRIV	PILGFRKIPM	PILSTLPETTV	PLHPAAMPHLL	PLLPIFFCLWV	PLIVLOAGFFL	PLPIHTAELLA	PLSYOHFRKIL	PMGVGI SPELL	PPAYBPNAPI	
Protein	æ	×	젒	8		2	젍	×	점	8	8	SP	8	젒	젍	젒	점	8	8	8	A A	젍	AB M	AB M	2	8	젒	젍	ğ	<b>%</b>	8	헟	전	텇	ರ್		<b>₩</b>	전	ಕ	2	점	NG NG	<b>%</b>	정	젚	2	3	

HBV B62 Super Motif

	SEQ ID NO:	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	. 2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	
	Conservancy (%)	80	90	80	95	7.5	80	100	06	0 <del>6</del> ;	06	7.5	100	95	95	100	95	100	7.5	80	85	98	90	95	80	06	85	95	80	98	80	95	80	80	95	100	95	. 82	100	100	ر د د	
	Sequence Frequency	16	18	16	19	15	16	20	18	18	18	15	20	19	19	20	19	20	15	16	17	19	18	19	16	18	17	19	16	19	16	19	16	. 91	19	20	19	17	20	20	6-	
uper Motif	No. of Amino Acids	11	11	11	11	11	11	11			=		-1	11	11		11	11	11	11	11	11	-11	-11		=		-	11	-				-11	-1-	-1	-1	-11	-1-	11	11	
HBV B62 Super Motif	Position	106	192	80	685	106	615	133	56	86	36	818	49	194	337	44	511	49	350	330	739	524	354	636	16	259	741	398	17	343	542	525	759	751	414	335	237	359	147	122	640	
	Sequence	POAMOWNSTTF	POSLDSWWTSL	CLDPARDVLCL	QVFADATPTGW	RLKLIMPARFY	RPIDWKVCORI	RPPNAPILSTL	ROALCWGELM	ROLLWFHISCL	RVAEDLNLGNL	RVHFASPLHVA	SIPWTHKVGNF	SLDSWMTSLNF	SILVPFVQWFV	SPEHCSPHHTA	SPFLLAGFTSA	SPHHTALROAI	SPTVWLSVIWM	SVRFSWLSLLV	SWLSRKYTSF	SVVRRAFPHCL	TPARVTGGVFL	TOCGYPALMPL	TVOASKLCLGW	· VLLDYGGMLPV	VLSRKYTSFPW	VPNLOSLTNLL	VOASKLCLGWL	VOWFVGLSPTV	VVLGAKSVOHL	WARAFPHCLA	WILRGTSFVYV	WLLGCAANWIL	WLSLDVSAAFY	WESLLVPFVQW	WMCLRRFIIFL	WMMWYWGPSLY	YLHTLWKAGIL	YLPLDKGIKPY	VPAI MPI VACI	
Table XIV	Protein	₽ N	PN BN	×	젍	젍	젙	3	2	3		젍	점	<b>№</b>	<b>№</b>	2	점	3	NG NG	<b>№</b>			전	ರ	3	<b>M</b>	젛	젒	S)	<u>~</u>	젙	ర్డ	점	점	젍	8	AB/A	Æ	전	ಕ	2	

## HBV A01 Motif with Binding Information

TABLE XV

Conservancy	Freq.	Protein	Position	Sequence	V	A*0101	SEQ ID NO:
100	20	Ø	166	ASFCGSPY	80		2028
06	18	ಶ	737	DNSVVLSRKY	10	0.0001	2029
95	19	점	631	FAAPFTOCGY	10	0.0680	2030
95	19	ರ	630	GFAAPFTQCGY	=		2031
75	15	SEC	140	GRETVLEY	<b>∞</b>		2032
85	17	점	579	GYSLNFMGY	6		2033
100	20	전	149	HTLWKAGILY	10	0.1100	2034
95	19	점	653	KQAFTFSPTY	0.	0.0001	2035
85	. 17	2	30	LLDTASALY	6	12.0000	2036
95	19	전	415	LSLDVSAAFY	0	0.0150	2037
75	15	SP	137	LTFGRETVLEY	=		2038
85	17	NG NG	360	MMWYWGPSLY	0	0.0810	2039
7.5	15	×	103	MSTTDLEAY	თ	0.8500	2040
06	18	ದ್ದ	738	NSVVLSRKY	6	0.0005	2041
100	20	정	124	PLDKGIKPY	6		2042
. 001	20	전	124	PLDKGIKPYY	10	0.1700	2043
85	17		797	PTTGRTSLY	o	0.2100	2044
100	20	점	165	SASFCGSPY	6		2045
95	19	전	416	SLDVSAAFY	6	5.2000	2046
7.5	15	×	104	STTDLEAY	80		2047
85	17	&	798	TTGRTSLY	80		2048
95	19	전	414	WLSLDVSAAFY	Ξ		2049
85	17	A B	359	WMMWYWGPSLY	Ξ	0.3200	2050
95	19	점	640	YPALMPLY	æ		2051
85	17		580	YSLNFMGY	8		2052

Table XVI HBV A03 Motif With Binding.

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
				-			
	•						
S	17	ᅙ	721	AACFARSR	æ	0.0004	2053
	17	전	721	AACFARSRSGA	=======================================		2054
	19	전	632	AAPFTQCGY	6		2055
95	19	전	632	AAPFTQCGYPA	=		2056
	17	PQ.	722	ACFARSRSGA	10		2057
	16	전	688	ADATPTGWGLA	=	-	2058
	18	Po	977	ADDPSRGR	<b>&amp;</b>		2059
		Ъ	529	AFPHCLAF	80		2060
	19	PQ.	529	AFPHCLAFSY	10		2061
	19	×	62	AFSSAGPCA	6		2062
	18	×	62	AFSSAGPCALR	=		2063
95	19	전	655	AFTFSPTY	æ		2064
	19	PQ.	655	AFTFSPTYK	6	0.2600	2065
	19	전	655	AFTFSPTYKA	10		2066
	19	전	655	AFTFSPTYKAF	=		2067
	16	EN	180	AGFFLTR	80		2068
	18	×	99	AGPCALRF	60		2069
	18	×	99	AGPCALRFTSA	=		2070
	19	P'OL	18	AGPLEEELPR	10	0.0004	2071
	19	전	521	AICSVVRR	æ	-0.0002	2072
	19	전	521	AICSVVRRA	6		2073
	19	전	521	AICSVVRRAF	10		2074
	19	ON	41	ALESPEHCSPH	=		2075
	18	전	772	ALNPADDPSR	10	0.0003	2076
	17	×	70	ALRFTSAR	80	0.0047	2077
	16	ENA	108	AMQWNSTTF	6		2078
	16	ENA	108	AMQWNSTTFH	10		2079
	15	×	102	AMSITDLEA	6		2080
	17	SIC NC	34	ASALYREA	80		2081
0	20	PQ.	166	ASFOGSPY	æ	0.0460	2082
80	16	전	822	ASPLHVAWR	6		2083
	15	EN	84	ASTINROSGR	6	0.000	2084
	16	진	069	ATPTGWGLA	6		2085
	16	5 J	755	CAANWILR	<b>&amp;</b>		2086
	19	×	61	CAFSSAGPCA	10		2087
	18	×	. 69	CALRFTSA	80		2088
	17	×	69	CALRFTSAR	<b>o</b>	0.0034	2089
	16	×	9	CCOLDPAR	æ		2090
	17	전	723	CFARSRSGA	6		2091

	Binding
X	With
Table	Motif
	A03
	HBV

	SeqID Num	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130
	A'0301							0.0083	0.0011			0.0029										0.0001	0.0042	0.0006	0.0004					-0.0009			0.0002	0.0082						
•	•																																			•				
	AA	တ	10	Ξ	6	<del>1</del>	=	. 11	<del>1</del>	80	0,	6	Ξ	80	10	Ξ	10	ω	80	10	æ	<del>1</del>	<b>=</b>	6	80	10	10	89	11	Ξ	80	80	6	Ξ	10	Ξ	G	10	<b>80</b>	Ξ
Dinaing																																								
AUS MOUIT WILL																																						•		
UDA AOS	Sequence	CFRKLPVNR	CGYPALMPLY	CGYPALMPLYA	CIPIPSSWA	CIPIPSSWAF	CIPIPSSWAFA	CLIFLLVLLDY	CLRPVGAESR	CLRRFIIF	CLARFIIFLE	CSPHHTALR	<b>CSPHHTALRQA</b>	CSWARAF	CSWRRAFPH	CTCIPIPSSWA	DATPTGWGLA	DDVVLGAK	DIDPYKEF	DIDPYKEFGA .	DLLDTASA	DLLDTASALY	DLLDTASALYR	DSWWTSLNF	DTASALYR	DTASALYREA	DVLCLRPVGA	DVSAAFYH	DVVLGAKSVQH	EAGPLEEELPR	EALESPEH	ELLAACFA	ELLAACFAR	ELLAACFARSR	ELLSFLPSDF	ELLSFLPSDFF	ESPEHCSPH	ESPEHCSPHH	ESALWDF	ESRLWDFSQF
	u C																															•								
	Position	607	638	638	312	312	312	253	17	239	239	48	48	523	523	310	689	540	31	31	53	53	59	196	35	32	14	418	541	17	40	718	718	718	43	43	43	43	374	374
	Protein	ᅙ	전	전	ENS	ENS	EVN	EN	×	ENS	ENA	SEC.	SE SE	P.	ᅙ	EN	S S	전	3	<b>S</b> C	SEC	3	SE SE	EN	3	SE SE	×	전	집	전	3	Po	ğ	PO	SE	2	SEC	SEC	징	Por
	y Freq.	15	19	19	20	20	16	19	18	19	15	20	20	19	19	20	16	18	18	18	17	17	17	19	17	16	19	19	18	19	18	18	18	17	19	19	19	19	19	19
	Conservancy	75	95	95	100	100	80	95	06	95	75	100	100	95	95	100	80	90	06	90	85	85	85	95	85	80	95	95	06	92	06	06	06	. 85	95	95	95	95	95	95



Table XVI HBV A03 Motif With Binding

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Conservancy	Freq.	Protein	Position	Sequence	АА	A'0301	SeqID Num
,							
92	19	2	174	ETTWRRR	80	0.0003	2131
80	16	SE	174	ETTWARRGR	10	0.0003	2132
95	19	전	631	FAAPFTQCGY	10		2133
85	17	POL	724	FARSRSGA	80		2134
80	16	PQ.	821	FASPLHVA	∞		2135
80	16	POL	821	FASPLHVAWR	10		2136
06	18	EN	13	FFPDHQLDPA	. 10		2137
85	17	EN	13	FFPDHQLDPAF			2138
75	15	SEC SEC	139	FGRETVLEY	6		2139
75	15	POL	244	FGVEPSGSGH	10		2140
95	19	SEC SEC	122	FGVWIRTPPA	10		2141
95	19	NC	122	FGVWIRTPPAY	=		2142
80	16	ENS	248	FILLLOLIF	6		2143
80	16	ENV	246	FLFILLCLIF	11		2144
75	15	ENV	171	FLGPLLVLQA	10		2145
95	19	POL	513	FLLAQFTSA	თ	90000	2146
95	19	Pol	562	FLLSLGIH	80		2147
95	19	EN	256	FLLVLLDY	80	0.0050	2148
100	20	정	363	FLVDKNPH	8		2149
92		Pol	658	FSPTYKAF	80		2150
95	19	×	. 63	FSSAGPCA	œ		2151
06	18	×	63	FSSAGPCALR	10		2152
06	18	×	63	FSSAGPCALRF	==		2153
100	20	ENV	333	FSWLSLLVPF	10	0.0004	2154
06	18	Po	536	FSYMDDVVLGA	=		2155
95	19	전	929	FTFSPTYK	8	0.0100	2156
95	19	전	929	FTFSPTYKA	თ		2157
92	19	POL	929	FTFSPTYKAF	10	0.0004	2158
92	19	Z Z	635	FTOCGYPA	80		2159
95	19	절	518	FTSAICSWR	10	0.0003	2160
95	19	<b>2</b> б	518	FTSAICSWRR	=	0.0065	2161
95	19	×	132	FALGGCRH			2162
06	18	×	132	PVLGGCPHK	<b>o</b>	0.0430	2163
06	18	정	. 992	FVYVPSALNPA	=		2164
80	16	집	754	GCAANWILR	6		2165
95	19	절	630	GFAAPFTOCGY	7		2166
06	18	EN	12	GFFPDHOLDPA	=		2167
75	15	EN	170	GFLGPLLVLOA	11		2168
85	17	ENC		GGLLGWSPQA	10		2169
			• .				

Table XVI HBV A03 Motif With Binding

				HBV AU3 Motif With Binding		٠	
Conservancy	Freq.	Protein	Position	Sequence	٨	A'0301	SeqID Num
100	20	절	360	GGVFLVDK	m		2170
100	20	절	360	GGVFLVDKNPH 1:	<b>=</b>		2171
75	15	전	267	GIHLNPNK	æ		2172
75	15	PO	267	GIHLNPNKTK 10	01	0.0025	2173
75	15	P.	267	GIHLNPNKTKR			2174
85	17	전	682	GLCQVFADA 9	<b>G</b>	0.0001	2175
95	19	<b>2</b> 0	627	GLIGFAAPF	o	9000.0	2176
85	17	EN	62	GLGWSPOA	6		2177
95	19	×	57	GLPVCAFSSA 10	10		2178
95	19	<u>P</u>	509	GLSPFLLA			2179
95	19	POL	509	GLSPFLLAQF 10	10	£	2180
85	17	NC C	29	GMDIDPYK 8	E E	9000.0	2181
85	17	SEC SEC	29	GMDIDPYKEF 10	10	-0.0003	2182
90	18	<b>2</b> 0	735		10	0.0010	2183
90	18	PQ.	735	<b>✓</b>		0.0140	2184
80	16	전	763		10		2185
80	16	전	245	GVEPSGSGH 9	on.		2186
100	20	POL	361	_	10		2187
80	16	POL	507		10		2188
95	19	SEC SEC	123	GVWIRTPPA 9	o.		2189
98	19	2	123		10	0.0047	2190
95	19	SEC SEC	123	œ		0.1900	2191
100	20	STC STC	47	HCSPHHTA 8			2192
100	20	SPC	47		10		2193
80	16	전	820		6		2194
80	16	POL	820	Œ	-		2195
. 56	19	×	49	HGAHLSLR 8	60		2196
85	17	EN	09	¥C.	-		2197
06	18	MC	104		6		2198
75	15	전	569		8		2199
75	15	집	<b>2</b> 69		6		2200
06	18	×	52	4	_		2201
80	16	짇	491	HLYSHPIILGF 1	=		2202
85	17	<u>S</u>	715		8		2203
85	17	전	715		10		2204
85	17	ğ	715		Ξ		2205
100	20	PQ.	149		0.	0.0440	2206
100	20	짇	149	¥	=	0.5400	2207
95	19	<u>ಕ</u>	522	ICSVVRRA 8	80		2208
			•				

Table XVI HBV A03 Motif With Binding.

				HBV AUS MOTH WITH BINGING		,	
Conservancy	Freq.	Protein	Position	Sequence	АА	A'0301	SeqID Num
30	Ģ	ā	000	7,407,41001			
ה נה	n (	<b>Ž</b> 2	275	ICOVARIATE CONTRACTOR	ה		5209
ກິດ	ۍ د -	된 된 :	522	ICSVVRRAFPH	Ξ.		2210
0.5	<b>10</b>	3	35	IDPYKEFGA	ກ		2211
06	18	Q	617	IDWKVCQR	8		2212
100	20	ENA	381	IFFCLWVY	∞		2213
95	19	ENA	255	IFLLVLLDY	ō		2214
80	16	PQ.	734	IGTDNSVVLSR	11		2215
100	. 50	EN	249	ILLICUF	8		2216
80	16	PQ.	760	ILRGTSFVY	თ	0.0440	2217
90	18	3	105	ISOLTFGR	8	0.0004	2218
90	18	전	625	IVGLLGFA	8		2219
06	18	전	625	IVGLLGFAA	6		2220
06	18	POL.	625	IVGLLGFAAPF	11		2221
100	20	ᅙ	153	KAGILYKR	8	0.0002	2222
80	16	전	503	KIPMGVGLSPF	11		2223
75	15	전	108	KLIMPARF	8		2224
75	15	PQ.	108	KLIMPARFY	6		2225
80	16	PQL	610	KLPVNRPIDWK	=		2226
85	17	PQ	574	KTKRWGYSLNF	1		2227
75	15	×	130	KVFVLGGCR	6	0.0420	2228
75	15	×	130	KVFVLGGCRH	10		2229
95	19	전	55	KVGNFTGLY	6	0.2100	2230
85	17	Pol	720	LAACFARSR	თ	0.0058	2231
95	19	×	16	LCLRPVGA	80		2232
06	18	×	16	LCLRPVGAESR	11.		2233
95	19	ğ	683	LCQVFADA	8		2234
100	20	POL	125	LDKGIKPY	8		2235
100	20	전	125	LDKGIKPYY	6		2236
80	16	×	ō	LDPARDVLCLR	11		2237
95	19	EN	195	LDSWWTSLNF	10		2238
85	17	2	31	LDTASALY	89		2239
85	17	2	31	LDTASALYR	6	0.0004	2240
80	16	3	31	LDTASALYREA	11		2241
95	19	PQ	417	LDVSAAFY	8		2242
92	19	전	417	LDVSAAFYH	6		2243
80	16	ENA	247		10		2244
92	19	전	544	LGAKSVQH	80		2245
80	16	전	753	LGCAANWILR	10		2246
75	15	절	266	LGIHLNPNK	თ		2247

Table XVI HBV A03 Motif With Binding

SeqID Num	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	. 2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	0077
A'0301				0.0022	-0.0002	0.0024			0.0013	0.0050				0.0230				9000'0				9000.0		0.0004						•	ě		-0.0009		0.0048			000	-0.0002
•																																							
AA	=	O	=	10	80	80	01	<b>σο</b>	6	10	=	æ	80	11	6	10	80	6	6	Ξ	œ	6	80	თ	10	=	Ξ	Ξ	10	Ξ	6	80	Ξ	6	10	=	80	Ξ •	0
ence	GIHLNPNKTK	LGPLLVLQA	LGPLLVLQAGF	/CLDY	LIMPARFY	LLAACFAR	LLAACFARSR	LLAQFTSA	LLDTASALY	SALYR	LLGCAANWILR	LLGFAAPF	LLGWSPQA	LLPIFFCLWVY	LLSFLPSDF	LLSFLPSDFF	LLVLQAGF	LLVLQAGFF	LLVPFVQWF	LLWFHISCLTF	LSFLPSDF	LSFLPSDFF	LSLDVSAA	LSLDVSAAF	LSLDVSAAFY	.SLDVSAAFYII	LSLGIHLNPNK	SLLVPFVQWF	LSLRGLPVCA	LSLRGLPVCAF	LSPFLLAQF	LSRKYTSF	LSTLPETTVVR	LSVPNPLGF	LSWLSLDVSA	LSWLSLDVSAA	LSYQI IFRK	LTFGRETVLEY	רו אומטוא
Sednence	LGIHLN	LGPLL	LGPLLV	LIFLLVLLDY	LIMP,	LLAA	LLAACI	LLAO	LLDT/	LLDTASALYR	LLGCA	LLGF	LLGW	LLPIFF	LLSFL	LLSFL	ורארנ	TLVLC	LLVPF	LLWFH	LSFL	LSFL	rsp	LSLD\	rsrdn	SACTST	LSLGIH	LSLLVP	LSLRG	LSLAGI	LSPFL	LSRK	LSTLPE	LSVP	rswrs	LSWLSI	rsya	LTFGRE	
Position	566	172	172	254	109	719	719	514	. 30	30	752	628	63	378	44	44	175	175	336	100	45	45	415	415	415	415	564	336	53	53	510	742	169	16	412	412	က	137	ה ה
Protein	POL	ENA	ENA	<b>™</b>	절	전	전	절	NC	3	전	전	<u></u>	ETV	3	3	EN	EN	ENA	3	3	3	집	전	전	전	전	ENS	×	×	전	전	SEC SEC	EN	ᅙ	Q	Pol	2 8	į
y Freq.	15	19	19	19	20	18	17	19	17	17	16	19	17	20	19	19	19	19	20	17	19	19	19	19	19	19	15	20	19	19	19	17	19	15	20	19	15	ភ ដ	2
Conservancy	75	95	95	95	100	06	85	95	85	85	80	95	85	100	95	92	98	95	100	85	95	95	92	95	95	95	75	100	95	95	95	9 5 85	95	75	100	100	92	75	œ œ

Table XVI HBV A03 Motif With Binding

SeqID Num	7866	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325
A'0301		0.0028		0.0016										0.0500		0.0008				-0.0002		-0.0009				9000'0	0.0020		0.0820	0.0008			0.0002						
AA	α.	, <b>c</b> o	6	<b>α</b> ο .	10	6	Ξ.	80	6	6	=	∞.	11	10	80	თ	10	Ξ	თ	80	10	=	10	=	6	80	6	<b>co</b>	თ	<b>o</b>	ω	10	თ	6	10	80	6	01	80
																											•												
9	ļ	· N	AR.	Ľ.	SR	<u>L</u>	÷	Ϋ́	AK	<b>H</b>	FGA	<b>*</b>	TLA TLA	SLY	EA.	ΑY	1YF	YFK	I	ж,	JH.	共	-GF	VSA	¥	¥	Κ̈́	E	关	æ	<b>(</b> 4	ISA	Ľ,	ΝF	GR	<b>₽</b>	SA	, AR	Ą
Sednence	I VI OAGEF	LVPFVQWF	LVSFGVWIR	LWDFSQF	LWDFSQFSR	MALPRIFIF	MALARFIIFLE	MDDWLGA	MDDWLGAK	MDIDPYKEF	MDIDPYKEFGA	MGVGLSPF	MGVGLSPFLLA	MMWYWGPSLY	MSTTDLEA	MSTTDLEAY	MSTTDLEAYF	MSTTDLEAYFK	NFLLSLGIH	NLEDPASR	NLNVSIPWTH	NLNVSIPWTHK	NLSVPNPLGF	NLSWLSLDVSA	NSOSPTSNH	NSVVLSRK	NSVVLSRKY	NVSIPWTH	NVSIPWTHK	PADDPSRGR	PALMPLYA	PAPCNFFTSA	PARDVLCLR	PARVTGGVF	PASTNROSGR	PAYRPPNA	PCALRFTSA	PCALRFTSAR	PCNFFTSA
Position	176	339	119	377	377	238	238	539	539	30	30	206	206	360	103	103	103	103	561	75	45	45	15	411	215	738	738	47	47	775	641	145	=	355	83	130	89	89	147
Protein	> 2 2	ENS	NC	PQL	전	ENA	ENA	절	절	NC S	ST ST ST ST ST ST ST ST ST ST ST ST ST S	젛	전	EN	×	×	×	×	짇	SEC C	절	절	EN	절	ENA	전	전	젛	절	절	ರ್	×	×	전	EN	SUC S	×	×	×
cy Freq.	67	20	18	20	20	19	15	18	18	18	18	16	16	17	16	15	15	15	19	18	19	19	15	18	15	18	18	20	20	18	19	15	16	18	15	19	18	17	15
Conservancy	56	001	06	100	100	95	75	06	06	06	06	80	80	85	80	75	75	75	95	06	95	95	95	06	75	06	06	100	100	06	95	75	80	06	75	95	06	85	75

Table XVI HBV A03 Motif With Binding.

SeqID Num	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364
A'0301		٠			0.0008	0.0048		0.0002	0.0011						0.0001	0.0002	0.0002			0.0012				-0.0002	0.0011	0.0002	0.0008		0.0001			0.0002	0.0310	0.0030	0.0450	•			
		i																																					
AA	∞	6	9	6	6	10	=	6	6	6	9	ထ	ω	თ	6	<del>1</del>	80	2	∞	<b>თ</b>	6	9	Ξ	80	თ	ω	თ	6	တ	10	ω	တ	6	တ	9	Ξ	თ	9	Ξ.
				٠																					-														
Sequence	PDHOLDPA	PDHQLDPAF	PFLLAGFTSA	PFTQCGYPA	PGYRWWCLR	PGYRWMOLPR	PGYRWMQLRRF	PIDWKVCQR	PIFFCLWVY	PIHTAELLA	PIHTAELLAA	PILGFRK	PIPSSWAF	PIPSSWAFA	PLDKGIKPY	PLDKGIKPYY	PLEEELPR	PLEEELPRLA	PLGFFPDH	PLHPAAMPH	PLLVLQAGF	PLLVLQAGFF	PLPIHTAELLA	PLSYQHFR	PLSYQHFRK	PLTVNEKR	PLTVNEKRR	PMGVGLSPF	PTTGRTSLY	PTTGRTSLYA	PVCAFSSA	PVGAESPGR	PVNRPIDWK	QAFTFSPTY	QAFTFSPTYK	QAFTFSPTYKA	QAGFFLLTR	QAMQWNSTTF	QAMQWNSTTFH
Position	15	15	512	634	233	233	233	616	380	713	713	496	314	314	124	124	20	20	10	427	174	174	711	2	2	98	86	505	797	797	59	20	612	. 654	654	654	179	107	107
Protein	ENV	EN	PQL	PQ.	ENA	ENA	ENV	POL	ENV	POL	Ē	PQ.	EN	EN	집	전	전	전	EN	전	EN	EN	전	전	전	PQ.	<u>g</u>	전	<u>5</u>	전	×	×	ᅙ	ᅙ	전	PO	EN	EN	ENC
Freq.	19	. 87	19	19	20	19	19	18	50	17	17	16	20	16	20	20	91.	16	19	20	19	19	16	20	15	17	17	16	17	17	19	18	17	19	19	19	16	16	16
Conservancy	95	. 06	95	95	100	95	95	06	100	85	85	80	100	80	100	100	95	06	06	100	95	95	80	100	75	85	85	80	85	85	95	06	85	95	95	95	80	80	80

Table XVI HBV A03 Motif With Binding.

	SeqID Num		2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403
	A'0301				-			0.0015	0.1200													0.0950				9000'0	0.2800	-0.0007					-0.0002	0.0054			0.0190	-0.0002	-0.0003	-0.0002	0.0058
	AA			7	=	80	80	6.	<b>.</b>	6	#	11	=	80	=	8	=	80	6	10	8	6	10	=	=	ō	-1	11	æ	6	Ξ	=	80	6	6	11	11	80	6	В	6
HBV AUS MOUIT WITH BINGING	Sequence		QCGYPALMPLY	QFTSAICSVVR	CSPRARRSCSR	QSSGILSR	RAFPHCLA	RAFPHCLAF	RAFPHCIAFSY	RDLLDTASA	RDLLDTASALY	RDVLCLRPVGA	RFSWLSLLVPF	RGLPVCAF	- RGLPVCAFSSA	RCASPAPA	RGTSFVVVPSA	PNGLLGF .	RIVGLLGFA	RIVGLLGFAA	RLKLIMPA	RLKLIMPAR	RLKLIMPARF	RLKLIMPARFY	RLKVFVLGGCR	RLVVDFSQF	ALVVDFSQFSR	RSPRARTIPSPR	RSCISPARA	RSCISPRIPR	RTPARVTGGVF	RTPPAYRPPNA	RIPSPRAR	RTPSPRARA	RVHFASPLH	RVHFASPLHVA	RVTGGVFIVDK	SAGPCALR	SAGPCALRF	SAICSVVR	SAICSVVRR
	Position		637	517	169	189	528	528	528	28	28	13	332	56	56	152	762	624	624	624	106	106	106	106	128	376	376	163	167	167	353	127	188	188	818	818	357	65	65	520	520
	Protein		ದ್ದ	절	2	POL	PQ.	ğ	절	NC CC	N.	×	ENS	×	×	NC NC	절	PQ	집	PQL	Z Z	절	전	PQ.	×	정	전	SEC S	SUC	SEC.	전	SE SE	SPC	SUC	전	전	전	×	×	전	Pol
	Conservancy Freq.		19	19	15	16	19	19	19	. 11	17	19	20	19	19	20	16	18	18	18	15	15	15	15	15	19	19	19	15	15	18	19	19	19	16	15	20	18	18	19	19
	Conserva	ļ	92	92	75	80	92	92	92	82	85	98	100	92	92	100	80	90	06	06	75	75	75	75	75	92	92	92	75	75	90	92	92	92	92	75	100	90	90	92	95

Table XVI HBV A03 Motif With Binding

	SeqID Num	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442
	A'0301			-0.0004										0.0016					0.0004	0.0080	-0.0003	0.0007	0.0150				9900'0		-0.0002		0.1100			9000'0						9000.0
Binding	АА	01		=	6	=======================================	80	6 .	10	8	=	=======================================	80	6	. 10	10	10	6	10	6	10	10		80	<b>80</b>	o	10	. 80	80	11	o	6	10	11	6	10	11	80	6	10
HBV AU3 Motif With Binding	Sequence	SAICSWRRA	SAICSWRRAF	SALNPADDPSR	SASFOGSPY	SFGVWIRTPPA	SFLPSDFF	SFPWUGCA	SFPWLLGCAA	SFVWPSA	SIPWTHKVGNF	SLDSWMTSINF	SLDVSAAF	SIQVSAAFY	SLDVSAAFYH	SIGIHLNPNK	SLLVPFVQWF	SLRGLPVCA	SLRGLPVCAF	SSAGPCALR	SSAGPCALRF	STIPETTVVR	STLPETTWRR	STNROSGR	STTDLEAY	STTDLEAYF	STTDLEAYFK	SVPNPLGF	SWLSRKY	SVVLSRKYTSF	SWARAFPH	TAELLAACF	TAELLAACFA	TAELLAACFAR	TASALYREA	TCIPIPSSWA	TCIPIPSSWAF	TDLEAYFK	TDNSVVLSR	TDNSVVLSRK
	Position	520	520	171	165	121	46	748	740	765	49	194	416	416	416	565	337	54	54	64	64	170	170	85	104	104	104	17	739	739	524	716	716	716	33	311	311	106	736	736
	Protein	PQ.	전	전	2	3	SPC	전	POL.	PQ.	전	EN	전	<u>S</u>	전	전	EN	×	×	×	×	ON.	SQ.	EN	×	×	×	EN	PQ.	POL	ď	PQ.	절	PQ.	SEC	ENA	ENA	×	전	POL
	Conservancy Freq.	19	19	18	20	. 18	19	15	15	16	20	19	19	19	19	15	20	19	19	18	18	19	19	16	. 15	15	15	15	18	17	19	17	17	17	16	20	20	16	18	18
	Conser	92	92	92	90	100	90	92	75	75	80	100	92	92	92	75	100	92	92	92	90	90	92	92	80	75	75	75	90	82	92	82	82	82	80	100	100	80	90	06

Table XVI HBV A03 Motif With Binding

SeqID Num	2443	2444	. 2445	2446	2447	2448	2449	2450	2451	2452	2453	2454	2455	2456	2457	2458	2459	2460	2461	2462	2463	2464	2465	2466	2467	2468	2469	2470	2471	2472	2473	2474	2475	2476	2477	2478	2479	2480	2481
A'0301					0.0007		0.0008	0.0007	0.0005	0.1300	5.3000	0.0082	0.0005	0.0018						9000.0	0.0004			0.0008	0.0003														
																	•		•									-											
AA	11	10	80	<b>თ</b>	<b>o</b>	9	<b>ი</b>	10	=	O	10	Ξ	σ	10	Ξ	10	Ξ	6	80	6	80	6	80	6	8	=	Ξ	=	8	6	80	Ģ	10	80	æ	10	6	=	80
																			•																	-			
Sequence	TDNSVVLSRKY	TFGRETVLEY	TFSPTYKA	TFSPTYKAF	TGGVFLVQK	TGRTSLYA	TLPETTVVR	TLPETTWRR	TLPETTWARR	TLWKAGILY	TLWKAGILYK	TLWKAGILYKR	TSAICSVVR	TSAICSWAR	TSAICSVVRRA	TSFPWLLGCA	TSFPWLLGCAA	TSFVYVPSA	TTDLEAYF	TTDLEAYFK	TTGRTSLY	TTGRTSLYA	TTSTGPCK	TTWARAGA	TWARAGA	TWARAGASPA	VCAFSSAGPCA	VOORNGLLGF	VDFSQFSR	VFLVDKNPH	VFVLGGCR	VFVLGGCRH	VFVLGGCRHK	VGAESPIGH	VGLLGFAA	VGLLGFAAPF	VGLSPFLLA	VGLSPFLLAQF	VGNFTGLY
Position	736	138	657	857	359	799	171	171	171	150	150	150	519	519	519	747	747	764	105	105	798	798	278	175	176	176	09	621	379	362	131	131	131	21	626	626	208	508	. 26
Protein	POL	SEC	전	전	전	전	3	3	SPC	전	전	전 전	ᅙ	ᅙ	ᅙ	전	ᅙ	PQ.	×	×	전	Po	ENA	3	SE SE	SE SE	×	전	전	전	×	×	×	×	전	Po	Po	Po	Po[-
/ Freq.	18	15	19	19	20	17	19	19	19	20	20	20	19	19	19	15	15	16	15	15	17	17	15	16	16	16	19	17	20	20	16	16	15	19	19	19	16	16	19
Conservancy	06	75	95	95	100	85	98	95	95	100	100	100	95	95	95	75	75	80	75	75	85	85	75	80	80	80	95	85	100	100	80	80	75	95	95	95	80	80	92

Table XVI HBV A03 Motif With Binding

				HBV A03 Motif With Binding			
Conservancy	Freq.	Protein	Position	Sequence	АА	A'0301	SeqID Num
85	17	互	96	VGPLTVNEK	6	0.0007	2482
85	17	전	96	VGPLTVNEKR	10		2483
85	17	집	96	VGPLTVNEKRR	=		2484
95	19	×	15	VLCLRPVGA	თ		2485
95	19	PQ.	543	VLGAKSVQH	თ		2486
06	18	×	133	VLGGCRHK	8	0.0150	2487
80	16	EN	177	VLQAGFFLLTR	11		2488
85	17	절	741	VLSRKYTSF	თ		2489
06	18	SEC C	120	VSFGVWIR	8	0.0040	2490
100	20	POL	48	VSIPWTHK	8	0.0130	2491
100	20	전	358	VTGGVFLVDK	10	0.0390	2492
100	20	PQ.	378	VVDFSQFSR	6	0.0015	2493
06	18	PQ	542	VVLGAKSVQH	10		2494
85	17	<u>S</u>	740	VVLSRKYTSF	10	0.0004	2495
95	19	<u>S</u>	525	VVRRAFPH	89		2496
95	19	PQ.	525	VVRRAFPHCLA	1		2497
80	16	NC S	177	WRREGRSPR	10	0.0027	2498
80	16	NC	177	WARAGASPAR	11		2499
06	18	NC NC	102	WFHISCLTF	6	٠	2500
06	16	ST.	102	WFHISOLIFGR	11		2501
85	17	SEC SEC	28	WGMDIDPY	89		2502
85	17	SEC C	28	WGMDIDPYK	6	-0.0003	2503
85	17	SEC.	28	WGMDIDPYKEF	11		2504
85	17	집	578	WGYSLNFMGY	10		2505
80	16	Ю	759	WILNGTSF	. 8		2506
80	16	Ю	759	WILAGTSFVY	10	0.0076	2507
95	19	SPC	125		89	-0.0002	2508
95	19	ž	125		6	0.0008	2509
06	18	전	314		8	-0.0002	2510
100	20	전	414	WLSLDVSA	8		2511
95	19	전	414	WLSLDVSAA	6		2512
95	19	집	414	WLSLDVSAAF	10		2513
95	19	집	414	WLSLDVSAAFY	11	0.0034	2514
100	20	EN	335		89		2515
85	17	5	26		10	0.0002	2516
85	17	2	56	×	=	0.0030	2517
95	19	EN	237		10	0.0004	2518
85	17	EN	359	WMMWYWGPSLY	11	6000.0	2519
100	20	ē	52	WTHKVGNF	œ		2520
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	Binding
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Table	Motif
	A03
	HBV

Conservancy	Freq.	Protein	Position	Sequence	AA	A'0301	SeqID Num
100	20	Pol	147	YLHTLWKA	80		2521
100	20	전	122	YLPLDKGIK	o	0.0001	2522
100	20	POL	122	YLPLDKGIKPY	=	-0.0004	2523
06	18	SE	118	YLVSFGVWIR	10	0.0005	2524
06	18	전	538	YMDDVVLGA	О	0.0001	2525
06	18	전	538	YMDDWLGAK	10	0.0330	2526
80	16	전	493	YSHPIILGF	6		2527
80	16	豆	493	YSHPIILGFR	10		2528
80	16	PQ.	493	YSHIPILGFRK	=		2529
85	17	전	580	YSLNFWGY	8	-0.0002	2530
75	15	전	746	YTSFPWLLGCA	=		2531
06	60	S	768	VVPSAINPA	σ		2532

Table XVII A11 Motif With Binding Information

121         AACFARSH         8         2533           322         AAPPICALKEY         9         2533           229         AFPICALKEY         10         2538           229         AFRICALKEY         11         2538           355         AFRIEDRA         11         2538           355         AFRIEDRA         11         2539           355         AFRIEDRA         11         2539           357         AFRIEDRA         10         2541           358         ACESPHONDSH         11         2541           357         ALESPHONDSH         11         2541           358         ACESPHONDSH         11         2541           359         ACESPHONDSH         11         2541           350         ACAMANDDSH         11         2541           350         ACASHARA         10         2541           350         ACAMANDDSH         10         2541           351         CAMANDSH         10         2541           352         CAMANDSH         11         2541           353         CALPIALLAN         11         2558           354         CAPAMANDSH         11	Protein
	POL 721
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2 0 8 0 0 8 0 0 1 1 0 0 1 8 0 1 1 8 0 1 1 8 0 1 1 1 8 0 1 1 1 1	
. 80 0 80 80 80 0 11 0 0 0 8 0 11 8 0 0 8 8 11 11 8 0 11	
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8 6 6 6 7 1 1 0 6 0 1 8 6 0 1 1 1 8 6 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	·
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8 6 6 11 6 6 6 7 8 6 6 11 8 6 6 11 8 6 6 11 11 11 11 11 11 11 11 11 11 11 11	ENV 84
8 8 9 11 01 8 8 9 11 11 8 8 9 11 11 8 9 11	POL 755
8 6 7 11 01 0 01 0 0 01 0 0 0 0 0 0 0 0 0 0	69 ×
e 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
01 01 8 01 11 8 9 01 8 8 11 11 8 9 11	
6 6 0 1 1 8 6 0 1 1 8 6 0 1 1 1 8 6 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ENV 253
01 01 01 01 88 81 11 11	
8 8 0.1 8 8 1.1 1.1 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	
01 8 8 0 11 11 8 0 11	
11 8 8 0 1 0 8 1 1 1 1 1 1 1 1 1 1 1 1 1	NUC 29
8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	NUC 29
0 0 8 8 1 1 1 1 8 8 0 1 1 1 1 1 1 1 1 1	POL 737
00 88 88 11 11 12 12 12 12 12 12 12 12 12 12 12	POL 737
8 8 T T 8 9 T	POL 737
88 TT 88 89 TT	NUC 32
## ## ## ## ## ## ## ## ## ## ## ## ##	POL 418
 80 1	
9 9	POL 17
6 1	NUC 40
=	POL 718

Table XVII A11 Motif With Binding Information

SeqiD Num	2541	2542	2543	2544	2545	2546	2547	2548	2549	2550	2551	2552	2553	2554	2555	2556	2557	2558	2559	2560	2561	2562	2563	2564	2565	2566	2567	2568	2569	2570	2571	2572	2573	2574	2575	2576	2577	2578	2579
A*1101																																							
АА	o	. 0	æ	10	10	10	<b>o</b> s	10	Ξ	æo`	œ	ဆ	10	80	10	Ξ	œ	O	o	Ξ	æ	=	æ	10	=	80	Ξ	10	=	တ	10	10	=	10	=	89	6	80	o
				•																																			
Sequence	ESPEHCSPH	ESPEHCSPHH	ETTWRRR	ETTWRRRGR	FAAPFTQCGY	FASPLHVAWR	FGRETVLEY	FGVEPSGSGH	FGVWIRTPPAY	FLLSLGIH	FLLVLLDY	FLVDKVPH	FSSAGPCALR	FTFSPTYK	FTSAICSVVR	FTSAICSWAR	FALGGORH	PALGGCRHK	GCAANWILR	GFAAPFTQCGY	GGVFLVDK	GGVFLVDKNPH	GIHLNPNK	GIHLNPNKTK	GIHLNPNKTKR	GMDIDPYK	GNLNVSIPWTH	GTDNSVVLSR	GTDNSVVLSRK	GVEPSGSGH	GVFLVDKNPH	GVWIRTPPAY	GVWIRTPPAYR	HCSPHHTALR	HFASPLHVAWR	HGAHLSLR	HISOLTFGR	HLNPNKTK	HLNPNKTKR
Position	43	. 4 . 60	174	174	631	821	139	244	122	562	256	363	63	656	518	518	. 132	132	754	630	360	360	267	567	267	29	44	735	735	245	361	123	123	47	820	49	104	569	569
Protein	SI N	O N	NC NC	NC	전	<u>5</u>	N N	절	2	절	ENA	Š	×	ğ	ğ	PQ.	×	×	<u>P</u>	ğ	절	절	<u>P</u>	PQ.	전	ST.	절	전	절	전	전	NC	ST.	NC	ğ	×	NC	절	전
Frequency	19	61	19	16	19	16	15	. 15	19	19	19	20	18	19	19	19	19	18	16	19.	20	20	15	15	15	17	19	18	18	16	20	19	19	20	16	19	18	15	15
Conservancy	95	9 S	98	80	95	80	75	75	95	98	95	100	06	92	95	95	95	06	80	95	100	100	75	75	75	85	95	06	06	80	100	95	95	100	80	95	06	75	75

Table XVII A11 Motif With Binding Information

SeqID Num	2580	2582	2583	2584	.2585	2586	2587	2588	2589	2590	2591	2592	2593	2594	2595	2596	2597	2598	2599	2600	2601	2602	2603	2604	2605	2606	2607	2608	5609	2610	2611	2612	2613	2614	2615	2616	2617	2618
A*1101																																						
A A	10	= =	; <b>co</b>	80	6	=	6	80	80	6	Ξ	6	10	o	6	Ξ	80	O)	<b>=</b>	80	o	80	6	80	10	ග	=	10	80	æ	10	O	10	Ξ	=	6	=	89
			:							-																												
Sequence	HTLWKAGILY	HILWKAGILYK	IDWKVCQR	IFFCLWY	IFLLVLLDY	IGTDNSVVLSR	(LRGTSFVY	ISQ.TFGR	KAGILYKR	KLIMPARFY	KLPVNRPIDWK	KVFVLGGCR	KVFVLGGCRH	KVGNFTGLY	LAACFARSR	LCLRPVGAESR	LDKGIKPY	LDKGIKPYY	LDPARDVLCLR	LDTASALY	LDTASALYR	LDVSAAFY	LDVSAAFYH	LGAKSVQH	LGCAANWILR	LGIHLNPNK	LGIHLNPNKTK	LIFLLVLLDY	LIMPARFY	LLAACFAR	LLAACFARSR	LLDTASALY	LLDTASALYR .	LLGCAANWILR	LLPIFFCLWVY	LNPADDPSR	LNPADDPSRGR	LNPNKTKR
Position	149	149	617	381	255	734	760	105	153	108	610	130	130	55	720	16	125	125	o	31	31	417	417	544	753	566	266	254	109	719	719	30	30	752	378	773	773	970
Protein	<u>5</u>	<u> </u>	<u> </u>	ENA	EN	절	정	NUC	POL	전	ğ	×	×	Z Z	ğ	×	절	전	×	NC	NC	<u>8</u>	ğ	<u>S</u>	PQ.	전	정	EN	절	전	전	200	NC	전	ENA	<u>S</u>	PQ.	정
Frequency	20	91	18	20	19	16	. 16	18	20	15	16	15	15	19	17	18	20	20	16	17	17	19	19	19	16	15	15	19	20	18	17	17	17	16	20	18	18	15
Conservancy	100	95	06	100	. 95	80	80	06	100	75	80	75	75	95	85	06	100	100	80	85	85	95	95	95	80	75	75	95	100	06	85	85	85	80	100	90	90	75

Table XVII A11 Motif With Binding Information

SeqID Num	2619	2620	2621	2622	2623	2624	2625	2626	2627	2628	2629	2630	2631	2632	2633	2634	2635	2636	2637	2638	2639	2640	2641	2642	2643	2644	2645	2646	2647	2648	2649	2650	2651	2652	2653	2654	2655	2656	2657
A*1101																																							
AA	11	=	10	. 10	11			80	=	80	6	10	o	10	6	Ξ	6		10.	=	6	80	6	80	6	6	6	10	10	6	10	6	6	∞	o	10	80	æ	o
Sednence	LNPNKTKRWGY	LNVSIPWTH	LNVSIPWTHK	LSLDVSAAFY	LSLDVSAAFYH	LSLGIHLNPNK	LSTLPETTVVR	LSYOHFRK	LTFGRETVLEY	LTVNEKRR	LVSFGVWIR	LWDFSQFSR	MDDVVLGAK	MMWWGPSLY	MSTTDLEAY	MSTTDLEAYFK	NFLLSLGIH	NLEDPASR	NLNVSIPWTH	NLNVSIPWTHK	NSOSPTSNH	NSVVLSRK	NSVVLSRKY	NVSIPWTH	NVSIPWTHK	PADDPSRGR	PARDVLCLR	PASTINFICISCR	PCALRETSAR .	PGYRWMCLR	PGYRWMCLPR	PIDWKVCQR	PIFFCLWVY	PILGFRK	PLDKGIKPY	PLDKGIKPYY	PLEEELPR	PLGFFPDH	РLНРААМРН
Position	570	46	46	415	415	564	169	ო	137	66	119	377	539	360	103	103	561	75	45	45	215	738	738	47	47	775	=	83	68	233	233	616	380	496	124	124	20	10	42.7
Protein	POL	전	절	절	절	PO	SE SE	전	NC C	전	NC	절	절	EN	×	×	젍	SAC SAC	절	전	ENA	ಕ್ಷ	ᅙ	전	전	정	×	ENA	×	EN	ËN	<u>R</u>	EN	전	절	<u>8</u>	전	<u>g</u>	Ъ
Frequency	15	19	19	19	19	15	19	. 15	15	17	18	20	18	17	15	15	19	18	19	19	15	18	18	20	20	18	16	15	17	20	19	18	20	16	20	20	19	19	20
Conservancy	75	95	95	95	95	75	95	75	75	85	06	100	06	85	75	75	92	06	98	95	75	06	06	100	100	06	80	75	85	100	95	06	100	80	100	100	95	98	100

Table XVII A11 Motif With Binding Information

SeqID Num	2658	2659	2660	2661	2662	2663	2664	2665	2666	2667	2668	2669	2670	2671	2672	2673	2674	2675	2676	2677	2678	2679	2680	2681	2682	2683	2684	2685	2686	2687	2688	2689	2690	2691	2692	2693	2694	2695	2696
A-1101																																							
¥ ¥	8	ത	80	<b>б</b> ъ	6	6	σ .·	6	6	10	6	10	11	=	1	80			80	6		11	11	Ξ	80	6	80	6	6		80	æ	6	11	o	6	10	10	တ
Sequence	PLSYOHER	PLSYOHFRK	PLTVNEKA	PLTVNEKRR	PNKTKRWGY	PTTGRTSLY	PVGAESHGR	PVNRPIDWK	QAFTFSPTY	QAFTFSPTYK	OAGFFLLTR	QAMQWNSTTFH	QCGYPALMPLY	QFTSAICSVVR	CSPRPRECSR	CSSGILSR	RAFPHCLAFSY	RDLLDTASALY	RG4SF4RR	RLKLIMPAR	RLKLIMPARFY	RLKVFVLGGCR	RLWDFSQFSR	RSPRRITPSPR	RSOSPARA	RSOSPRARR	RIPSPARR	RIPSPRRR	RVHFASPLH	RVTGGVFLVDK	SAGPCALR	SAICSVVR	SAICSVVRR	SALNPADDPSR	SASFOGSPY	SLDVSAAFY	SLDVSAAFYH	SLGIHLNPNK	SSAGPCALR
Position	. 2		86	86	572	797	20	612	654	654	179	107	637	517	169	189	528	28	152	106	106	128	376	183	167	167	188	188	818	357	<b>6</b> 9	520	520	171	165	416	416	565	64
Protein	정	ē		전	전	전	×	<u>8</u>	정	<u>8</u>	ENA	ENA	전	전	SPC	전	전	2	SPC	ğ	<u>8</u>	×	전	2	SPC	SP	SE	SE SE	전	절	×	Ą	절	PQ.	<u>S</u>	전	절	정	×
Frequency	20	15	17	17	15	17	18	. 17	19	19	16	16	19	19	15	16	19	17	20	15	. 15	15	19	19	15	15	19	19	16	50	18	19	19	18	50	19	19	15	18
Conservancy	100	75	85	85	75	85	06	85	98	95	80	80	92	95	75	80	95	85	100	75	75	75	98	95	75	75	95	95	80	100	06	95	95	06	100	95	95	75	06

Table XVII A11 Motif With Binding Information

Frequency Protein	Prote	. <u>c</u>	Position	Sednence	A A	A-1101	SeqID Num
			1		Ç		2692
19 NAC 1/0	•	0/1		SILPETIVA	) <del>,</del>		803
16 ENV 85		85		STINGSGR	<u> </u>		2699
_		104		STTDLEAY	<b>co</b>		2700
15 X 104		104		STTDLEAYFK	10		2701
18 POL 739		739		SVVLSRKY	8		2702
		524		SWRRAFPH	<b>თ</b>		2703
		716		TAELLAACFAR	11		2704
		106		TDLEAYFK	σ		2705
<u>7</u>		736		TDNSVVLSR	<b>o</b>		2706
Pol		736		TDNSVVLSRK	10		2707
	•	736		TDNSVVLSRKY			2708
NUC		138		TFGRETVLEY	10		2709
		359		TGGVFLVDK	6		2710
		171		TLPETTVVR	O		2711
		171		TLPETTVVRR	10		2712
	•	171		TLPETTVVRRR	=		2713
		150		TLWKAGILY	6		2714
		150		TLWKAGILYK	10		2715
		150		TLWKAGILYKR	11		2716
POL		260		TNFLLSLGIH	10		2717
<b>.</b>		519		TSAICSVVR	ກ <sup>(</sup>		2718
Z		519		ISAICSVVRH	<u> </u>		9172
		105		IIDLEAYFK	<b>න</b>		2721
		736		TISTGPCK	. w		2722
		175		TTWARAGA	· 6		2723
NC		176		TWRARGR	80		2724
		176		TWRRAGRSPR	11		2725
		379		VDFSQFSR	80		2726
•		362		VFLVDKNPH	6		2727
		131		VFVLGGCR	89		2728
		131		VFVLGGCRH	6		2729
15 X 131		131		VFVLGGCRHK	10		2730
		12		VGAESHGR	80		2731
		99		VGNFTGLY	80		2732
POL		96		VGPLTVNEK	6		2733
17 POL 96		96		VGPLTVNEKR	10		2734
17 POL 96		96		VGPLTVNEKRR	=		2735

Table XVII
A11 Motif With Binding Information

			<u>-</u>	A11 Motif With Binding Information			
Conservancy	Frequency	Protein	Position	Sequence	АА	A*1101	SeqID Num
40	6	Ca	543	HONSARO IN	·		2736
8 6	8 7	· -	133	AHBOOD IV	o cc		2737
) (	5 1	K W	177	VLOAGEFILTB	· =		2738
85	17	전	613	VNRPIDWK	ω		2739
06	18	MC	120	VSFGVWIR	æ		2740
100	20	<u>8</u>	48	VSIPWTHK	80		2741
100	20	Ž	358	VTGGVFLVDK	10		2742
100	. 20	ğ	378	WDFSQFSR	o		2743
06	18	<u>S</u>	542	VVLGAKSVQH	10		2744
95	19	<u>S</u>	525	WARAFPH	æ		2745
80	16	SPC	177	WARRGASPR			2746
80	16	SPC SPC	177	WARAGRSPAR	=		2747
06	18	SPC SPC	102	WFHISCLIFGR	=		2748
85	17	SPC SPC	. 58	WGMDIDPY	æ		2749
85	17	N.C.	28	WGMDIDPYK	o		2750
85	17	P	578	WGYSLNFWGY	10		2751
80	16	절	759	WILBGTSFVY	9		2752
95	19	NC	125	WIRTPPAY	80		2753
95	19	NC	125	WIRTPPAYR	Ø		2754
06	. 81	P	314	WLQFRNSK	æ		2755
95	19	POL	414	WLSLDVSAAFY	Ξ		2756
85	17	SPC SPC	26	WLWGMDIDPY	10		2757
85	17	SPC	26	WLWGMDIDPYK	Ξ		2758
85	17	EN	359	WMMWWGPSLY	=		2759
100	20	전	122	YLPLDKGIK	o		2760
100	20	<u>8</u>	122	YLPLDKGIKPY	Ξ		. 2761
06	18	NC	118	YLVSFGVWIR	01		2762
06	18	절	538	YMDDVVLGAK	10		2763
80	16	절	493	YSHPILGFR	10		2764
80	16	절	493	YSHPIILGFRK	=		2765
85	17	전	580	YSLNFWGY	<b>&amp;</b>		2766

0.0004 0.0012 0.0310 0.0024 A\*2401 0.0007 Filed A A HBV A24 Motif With Binding Information SEQ ID 2772 2773 2774 2775 2776 2777 2778 2779 2779 2780 2781 2783 2802 2803 2804 2805 ÿ FFPDHQLDPAF GFFLLTRI HYLHTLWKAGI IFFCLWVYI **AFTFSPTYKAF** DYGGMLPVCPL EYLVSFGVW EYLVSFGVWI GYRWMCLRRF GYRWMCLRRFI **HFASPLHVAW** WMMWWGPSI DWKVCQRIVGL GFFLLTRIL GFFLLTRILTI GFFDHOL GYSLNFMGYVI CFRKLPVNRPI GFRKIPMGVGL AFSSAGPCAL AFSYMDDVVL GWSPQAQGIL KFAVPNLOSL **AMQWNSTTF** AYRPPNAPI AYRPPNAPIL FFCLWYI FFLLTRIL GMDIDPYKEF GWSPOAGGI GWLWGMDI DWKVCQRI FFLLTRILTI GFIGPLLM GMLPVCPL GYPALMPL FLFILLCL KYTSFPWL FLFILL HFRKILLL Sequence Position 117 382 182 182 181 12 170 500 29 265 25 65 65 639 234 234 234 234 820 181 Protein Freq. Table XVIII Conservancy 

Sequence   Fieel,   Protein   Position   Sequence   NO.   AA   Filed   A-Z									•
17   POL	Conservancy	Freq.	Protein	Position	Sequence	SEQ ID NO:	AA	Filed	A*2401
16   BW   247   UFILLCL   2811   8	8. 7.	17	Ø	745	KYTSFPWLL	2810	6	٠	5.3000
16   BW   247   UPILLCUE   2815   9	80	16	2	247	LFILLCL	2811	- αο		
16   BW   247	80	16	8	247	LFILLICLI	2812	σ		
16   BW   247   LFILLCLIF   2814   11     19   PQL   643   LMPHISOL   2815   8     17   NUC   101   LWPHISOL   2816   10     16   PQL   492   LYSHPHILGF   2819   10     17   BW   360   MMYWGPSL   2820   9     17   BW   360   MMYWGPSL   2821   9     18   PQL   561   NMLISCHIF   2822   11     19   PQL   561   NMLISCHIF   2822   11     19   PQL   561   PMLISCHIF   2822   11     19   PQL   561   PMLISCHIF   2822   11     19   PQL   561   PMLISCHIF   2822   11     19   PQL   563   PMCNISTSPH   2826   11     19   PQL   565   PMCNISTSPH   2822   11     10   PQL   565   PMCNISTSPH   2822   11     10   PQL   565   PMCNISTSPH   2822   11     10   PQL   565   PMCNISTSPH   2822   11     10   PQL   565   PMCNISTSPH   2822   11     10   PQL   565   PMCNISTSPH   2823   11     10   PQL   565   PMCNISTSPH   2832   11     10   PQL   565   PMCNISTSPH   2832   11     10   PQL   565   PMCNISTSPH   2832   11     10   PQL   565   PMCNISTSPH   2834   11     10   PQL   565   PMCNISTSPH   2834   11     11   PQL   572   PFINITFILL   2835   8     12   PMN   242   PFINITFILL   2835   8     13   PROMOSLINFF   2844   10     14   PMN   236   PMCNISTSPH   2844   11     15   PMN   236   PMCNISTSPH   2845   11     16   PQL   46   SPLOSDFT   2845   11     17   PQL   413   SWISLINFF   2845   11     18   PQL   413   SWISLINFF   2845   11     19   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2845   11     10   PQL   413   SWISLINFF   2	08	16	20	247	LFILLCLIF	2813	10		
19   PCL   643   UMPLYACI   2815   8	80	16	8	247	LFILLICLIFL	2814	=		
18   NLC   101   UVPHISCL   2816   8	95	19	전	643	LMPLYACI	2815	œ		
17   NLC   101   LVM-HISCLIT   2817   10     16   POL   492   LVS-HPILGF   2819   10     17   BM   361   MANYWGPSL   2820   9   9     17   BM   361   MANYWGPSL   2820   9   9     19   POL   561   NFLISIGH   2823   10     19   POL   561   NFLISIGH   2823   10     19   POL   561   NFLISIGH   2823   10     19   POL   561   NFLISIGH   2823   11     19   POL   562   PMGVGLSPH   2826   11     10   POL   505   PMGVGLSPH   2827   9     10   POL   505   PMGVGLSPH   2827   9     10   POL   505   PMGVGLSPH   2828   11     10   POL   505   PMGVGLSPH   2829   10     10   POL   505   PMGVGLSPH   2831   11     10   POL   505   PMGVGLSPH   2831   11     10   POL   505   PMGVGLSPH   2832   11     11   POL   505   PMGVGLSPH   2831   11     12   POL   510   PMLLGCANNW   2831   11     10   POL   510   PMLLGCANNW   2832   11     11   POL   510   PMLLGCANNW   2832   11     12   PW   242   PHIFFILL   2833   8     13   PMMCGRSPH   2834   11     14   PWM   242   PRIFFILL   2833   8     15   PW   242   PRIFFILL   2834   11     16   POL   577   PMGCRSPH   2841   11     17   POL   577   PMGCRSPH   2841   11     18   PW   236   PMGCRSPH   2842   11     19   PW   236   PMGCRSPH   2845   11     10   PUL   446   SPCRSPVSM   2846   9     11   POL   446   SPCRSPVSM   2846   9     12   POL   446   SPCRSPVSM   2846   9     13   PUL   546   SPCRSPVSM   2846   9     14   POL   446   SPCRSPVSM   2846   9     15   PUL   334   SWMCSLMPR   2850   10     16   POL   445   SWMCSLMPR   2850   10     17   POL   446   SPCRSPVSM   2846   9     18   POL   446   SPCRSPVSM   2846   9     19   POL   445   SWMCSLMPR   2850   9     10   POL   446   SPCRSPVSM   2846   9     11   POL   445   SWMCSLMPR   2850   9     12   POL   446   SPCRSPVSM   2846   9     13   SWMCSLMPR   2850   9     14   POL   446   SPCRSPVSM   2846   9     15   POL   447   SWMCSLMPR   2850   9     10   POL   448   SWMCSLMPR   2850   9     10   POL   448   SWMCSLMPR   2850   9     10   POL   448   SWMCSLMPR   2850   9     10   POL   446   SWMCSLMPR   2850   9     10   POL   448   SWMCSLMPR   28	90	18	NC	101	LWFHISCL	2816	80		
16   POL   492   LYSHPIIL   2818   8   1   1   1   1   1   1   1   1	85	17	SAC NC	101	LWFHISCLTF	2817	10		
16   POL   492   Livishilidis   2219   10	80	16	전	492	LYSHPIIL	2818	ω		
17   BW 360   MMYWGPSL 2820   9   1   1   1   1   1   1   1   1   1	80	16	젌	492	LYSHPIILGF	2819	10	•	1.1000
17         BW         361         MWWGPSL         2821         8           19         POL         561         NFLLSLGIH         2822         8           19         POL         561         NFLLSLGIH         2823         10           19         POL         561         NFLLSLGIH         2824         9           19         POL         512         PFLLALOFTSAI         2826         11           19         POL         512         PFLLALOFTSAI         2826         11           19         POL         512         PFLLALOFTSAI         2826         11           16         POL         505         PMCMCGNPRIT         2826         11           16         POL         505         PMCMCGSPPL         2829         11           16         POL         505         PMCMCGSPPL         2829         11           16         POL         505         PMCMCGSPPL         2829         11           16         POL         505         PMCGCAPAIN         2833         9         11           16         POL         505         PMCGCASPAIN         2833         9         11           16         POL<	85	17	<b>8</b>	360	MMWYWGPSL	2820	თ	•	0900'0
19   P.O.   561   NPLESIGH   2822   8   8   8   8   1   9   P.O.   561   NNLHAGISH   2823   10   10   10   10   10   10   10   1	85	17	8	361	MWYWGPSL	2821	œ		0.0005
19         POL         561         NFLISIGHL         2823         10           16         POL         578         NWILLAGTSF         2825         11           19         POL         512         PFLLAGTSF         2825         11           19         POL         503         PROMONTGAL         2826         10           16         POL         505         PMGVGLSPF         2829         9           16         POL         505         PMGVGLSPF         2829         10           16         POL         505         PMGVGLSPF         2829         10           16         POL         505         PMGVGLSPF         2829         10           16         POL         505         PMGVGLSPF         2829         11           16         POL         50         PMCGLSPF         2829         11           16         POL         50         PMCGCLSPF         2839         11           16         POL         51         PMCGCANWI         2833         9         11           15         BN         242         PFFIFFFILL         2835         8         11           15         BW <t< td=""><td>95</td><td>19</td><td>젒</td><td>561</td><td>NFLLSLGI</td><td>2822</td><td>80</td><td></td><td></td></t<>	95	19	젒	561	NFLLSLGI	2822	80		
16         POL         758         MWINGTISF         2824         9           19         POL         512         PFLIACTSNPAL         2826         11           19         POL         634         PFLOGATPAL         2826         10           19         POL         505         PMGVGLSPFL         2829         10           16         POL         505         PMGVGLSPFL         2829         10           16         POL         505         PMGVGLSPFL         2829         10           16         POL         505         PMGVGLSPFL         2839         11           16         POL         50         PMCVGLSPFL         2830         11           20         POL         50         PMCCGLSPFL         2830         11           19         BM         242         PMTHCGLSPFL         2833         11           15         BW         242         PRIFIEFIL         2836         11           15         BW         242         PRIFIEFIL         2836         11           16         BW         242         PRIFIEFIL         2836         11           16         BW         242         PRIFIEF	95	19	젌	561	NFLLSLGIHL	2823	10		0.0099
19         POL         \$12         PFLLAGGYPAL         2825         11           19         POL         \$34         PFTGGGYPAL         2826         10           19         BW         341         PPWGWFGL         2829         10           16         POL         \$05         PMGGGSPH         2829         10           16         POL         \$05         PWGGGSPH         2829         10           16         POL         \$05         PWGGGSPH         2829         10           16         POL         \$05         PWGGGSPH         2829         10           16         POL         \$150         PWLIGCAMW         2831         11           16         POL         \$15         PWLIGCAMW         2832         11           19         BW         \$24         PWILLGCAMW         2833         11           19         BW         \$24         PWILLGCAMW         2836         9         11           15         BW         \$24         PWILLGCAMW         2836         11         11           15         BW         \$24         PRIFIEFILL         2836         11           15         BW	80	16	전	758	NWILRGTSF	2824	<b>o</b>		
19         POL         634         PFTOGGYPAL         2826         10           19         BW         341         PPTOGGYPAL         2827         9           16         POL         505         PMGVGLSPF         2829         10           16         POL         505         PMGVGLSPFL         2829         10           16         POL         505         PMGVGLSPFL         2829         10           16         POL         50         PMGVGLSPFL         2829         10           16         POL         50         PMGVGLSPFL         2830         11           20         POL         51         PMLGGANW         2832         11           19         BW         242         PRIFICH         2833         9         7           15         BW         242         PRIFICH         2836         9         11           15         BW         242         PRIFICH         2836         9         1           15         BW         242         PRIFICH         2836         1         1           15         BW         242         PRIFICH         2836         1         1           <	98	19	පු	512	PFLLAQFTSAI	2825	=		
19         BW         341         PRYOWRYGI.         2827         9           16         POL         505         PMGVGLSPFL         2828         9           16         POL         505         PMGVGLSPFL         2828         9           16         POL         505         PMGVGLSPFL         2828         10           16         POL         505         PMGVGLSPFL         2830         11           20         POL         51         PMTLGCAANW         2831         10           19         BW         242         PMTLGCAANW         2833         8           15         BW         242         PMTLGCAANW         2833         8           15         BW         242         PMTLGCAANW         2833         8           15         BW         242         PMTLGCAANW         2835         9           15         BW         242         PMTLGCAANW         2833         11           16         BW         242         PMTLGCAANW         2835         9           16         BW         242         PMTRGLFILL         2833         11           16         BW         242         PMTSGLFILL	98	19	젍	634	PFTQCGYPAL	2826	10		0.0002
16         POL         505         PMGVGLSPF         2828         9           16         POL         505         PMGVGLSPFL         2829         10           16         POL         505         PMGVGLSPFL         2830         11           16         POL         750         PWLLGCAANWI         2831         11           20         POL         51         PWLLGCAANWI         2832         11           19         BAW         242         PMTHKVGNF         2833         1           15         BAW         242         PFIFILFILL         2836         1           15         BAW         242         PFIFILFILL         2836         1           20         BAW         242         PFIFIFFILL         2836         1           20         BAW         242         PFIFIFFILL         2836         1           20         BAW         332         PFSWLSLL         2836         1           20         BAW         332         PRWCNSLMF         2842         8           19         BAW         236         PRWCLARPF         2842         1           19         BAW         236         PRWCLARPF <td>95</td> <td>19</td> <td><u>M</u></td> <td>341</td> <td>PFVQWFVGL.</td> <td>2827</td> <td>თ</td> <td></td> <td>0.0003</td>	95	19	<u>M</u>	341	PFVQWFVGL.	2827	თ		0.0003
16         POL         505         PMONGLSPFL         2829         10           16         POL         505         PMULGCAANW         2830         11           16         POL         750         PWLLGCAANW         2832         11           20         POL         51         PWTHKVGNF         2833         9         -           19         BN         242         PRIFICH         2836         9         -           15         BW         242         PRIFICH         2836         9         -           20         BW         324         PRIFICH         2836         9         -           21         BW         242         PRIFICH         2838         11           20         BW         332         PRWANZSLIVF         2840	80	16	전	505	PMGVGLSPF	2828	თ		
16         POL         505         PMGVGLSPFLL         2830         11           16         POL         750         PWLLGCAANW         2831         10           16         POL         51         PWLLGCAANW         2832         11           20         POL         51         PWLLGCAANW         2832         11           19         BN         242         PFIFIE         2833         9           15         BN         242         PFIFIE         2835         8           15         BN         242         PFIFIE         2836         8           15         BN         242         PFIFIE         2836         8           15         BN         242         PFIFIE         2836         11           20         BN         232         PFSMLSLLPF         2839         8           17         POL         577         PMGYSHFF         2840         11           19         BN         236         RWACLRFFI         2843         9         1           19         BN         236         RWACLRFFI         2843         9         1           10         BN         236         R	80	16	젒	505	PMGVGLSPFL	2829	10		
16         POL         750         PWLLGCAANW         2831         10           16         POL         51         PWLLGCAANW         2832         11           20         POL         51         PWTHKVGNF         2833         11           15         BW         242         RFIIFLFI         2835         8           15         BW         242         RFIIFLFIL         2836         9           15         BW         242         RFIIFLFIL         2836         9           15         BW         242         RFIIFLFIL         2836         9           15         BW         242         RFIIFLFILL         2836         9           20         BW         332         RFSWLSLL         2838         11           20         BW         332         RFSWLSLLYF         2840         11           19         BW         236         RWACJSLNF         2841         8           19         BW         236         RWACJSLNF         2843         9         .           19         BW         236         RWACJSLNF         2845         11         .           20         BW         236	80	16	젍	505	PMGVGLSPFLL	2830	=		
16         POL         750         PWLLGCAAWWI         2832         11           20         POL         51         PWTHKNGNF         2833         9         .           19         BNV         242         RFIIFLFIL         2835         8         .           15         BNV         242         RFIIFLFILL         2836         9         .           15         BNV         242         RFIIFLFILL         2836         9         .           20         BNV         332         RFSWLSLYPF         2840         11         .           20         BN         236         RWANCLRRF         2842         9         .           19         BN         236         RWANCLRRF         2845         11         .           20         <	80	16	텇	750	<b>PWLLGCAANW</b>	2831	01		
20         POL         51         PWTHKNGNF         2833         9         .           19         BW         344         QWPGLSPTW         2834         11         .           15         BW         242         RFIIFLFIL         2835         8         .           15         BW         242         RFIIFLFILL         2836         11           15         BW         242         RFIIFLFILL         2836         11           20         BW         242         RFIIFLFILL         2836         11           20         BW         332         RFSWLSIL         2836         11           17         POL         577         RWGYSINF         2840         11           19         BW         236         RWMCLRRF         2842         8           19         BW         236         RWMCLRRF         2843         9         .           19         BW         236         RWMCLRRF         2844         10         .           20         POL         167         SFCGSPYSW         2846         9         .           19         BW         236         RWMCSLLVPF         2846         11	80	. 16	ಶ	750	<b>PWLLGCAANWI</b>	2832	Ξ		
19         BNV         344         OWFVGLSPTWW         2834         11           15         BNV         242         RFIIFLFIL         2835         8           15         BNV         242         RFIIFLFILL         2836         9           15         BNV         242         RFIIFLFILL         2838         11           20         BNV         332         RFSWLSLLYPF         2840         11           17         DOL         577         RWGYSLNF         2840         11           19         BN         236         RWMCLRRF         2842         8           19         BN         236         RWMCLRRF         2842         8           19         BN         236         RWMCLRRF         2843         9         *           19         BN         246         SFCGSPYSW         2845         11         *	100	20	젍	51	PWTHKVGNF	2833	თ	•	0.0290
15         BNV         242         RFIIFLFIL         2835         8           15         BNV         242         RFIIFLFILL         2836         9           15         BNV         242         RFIIFLFILL         2838         11           20         BNV         332         RFSWLSLL         2839         8           20         BNV         332         RFSWLSLL         2840         11           19         BNV         236         RWMCYSLNF         2842         8           19         BNV         236         RWMCLRRFI         2843         9         1           19         BNV         236         RWMCLRRFI         2844         10         1           19         BNV         236         RWMCLRRFI         2845         11         1           19         BN         236         RWMCLRRFI         2845         11         1           19         NLC         46         SFUSSEYSW         2846         9         1           19         POL         765         SFVYNPSAL         2849         11         1           20         BN         334         SWMTSLLYPF         2850         9	98	19	AG	344	OWFVGLSPTVW	2834	=		
15         BNV         242         RFIIFLFILL         2836         9           15         BNV         242         RFIIFLFILL         2838         11           20         BNV         332         RFSMLSLL         2839         8           20         BNV         332         RFSMLSLLVPF         2840         11           20         BNV         236         RVMCLRRFI         2842         8           19         BNV         236         RVMCLRRFI         2843         9         *           19         BNV         236         RVMCLRRFI         2844         10         *           19         BNV         236         RVMCLRRFI         2845         11         *           19         BNV         236         RVMCLRRFI         2845         11         *           10         NLC         46         SFCGSPYSW         2846         9         *           10         NLC         46         SFUSDIA         2845         11         *           10         POL         413         SWLSLUVFSAF         2849         11         *           20         BNV         334         SWPKFAVPI         2850<	75	15	8	242	RFIIFLFI	2835	89		
15         BNV         242         RFIIFLFILL         2837         10           15         BNV         242         RFIIFLFILL         2838         11           20         BNV         332         RFSWLSLLWF         2840         11           20         BN         332         RFSWLSLLWF         2841         8           17         POL         577         RWACYSINF         2841         8           19         BN         236         RWACLARFI         2843         9         *           19         BN         236         RWACLARFI         2844         10         *           19         BN         236         RWACLARFI         2845         11         *           19         BN         236         RWACLARFI         2845         11         *           19         BN         46         SFLPSDF         2845         11         *           10         POL         46         SFLPSDF         2846         9         *           10         POL         46         SFLPSDF         2848         9         *           20         BN         334         SWISLLVP         2850         <	75	15	<b>№</b>	242	RFIIFLFIL	2836	6		
15         BNV         242         RFIFLILL         2838         11           20         BNV         332         RFSWLSLL         2839         8           20         BNV         332         RWACLRRF         2840         11           17         POL         577         RWACLRRF         2842         8           19         BNV         236         RWACLRRF         2843         9         *           19         BNV         236         RWACLRRF         2844         10         *           20         POL         167         SFCGSPYSW         2846         9         *           19         NLC         46         SFLPSDF         2845         11         *           19         POL         46         SFVYVPSAL         2848         9         *           19         POL         413         SWLSLVPF         2849         11         *           20         BW         334         SWLSLVPF         2850         9         *           20         BW         334         SWMTSLNF         2851         10         *           20         BW         197         SWWTSLNF         2852<	75	15	8	242	RFIIFLFILL	2837	10		
20         BNV         332         RFSWLSLL         2839         8           20         BNV         332         RFSWLSLLVPF         2840         11           17         POL         577         RWACLRRF         2841         8           19         BNV         236         RWACLRRFI         2843         9         *           19         BNV         236         RWAMCLRRFII         2844         10         *           20         POL         167         SFCGSPYSW         2846         9         *           19         NUC         46         SFLPSDFF         2848         9         *           16         POL         765         SFVYVPSAL         2848         9         *           19         POL         413         SWLSLVPF         2849         11         *           20         BW         334         SWLSLVPF         2850         9         *           20         BW         334         SWMTSLNF         2851         10         *           20         BW         197         SWWTSLNF         2852         8         *	75	15	8	242	RFIIFLFILL	2838	=		
20         BNV         332         RFSWLSLLVPF         2840         11           17         POL         577         RWGYSLNF         2841         8           19         BNV         236         RWMCLRRFI         2843         9         *           19         BNV         236         RWMCLRRFII         2844         10         *           20         BNV         236         RWMCLRRFIIF         2845         11         *           20         POL         167         SFCGSPYSW         2846         9         *           19         NUC         46         SFLPSDFF         2848         9         *           16         POL         765         SFVYVPSAL         2848         9         *           19         POL         413         SWLSLLVPF         2849         11         *           20         BW         334         SWLSLLVPF         2850         9         *           20         BW         197         SWMTSLNF         2852         8         *           20         BW         197         SWMTSLNF         2852         8         *	100	20	AB M	332	RFSWLSLL	2839	œ		
17         POL         577         RWGYSLNF         2841         8           19         BNV         236         RWMCLRRFI         2842         8         •           19         BNV         236         RWMCLRFII         2844         10         •           20         POL         167         SFCGSPYSW         2846         9         •           19         NUC         46         SFLPSDFF         2847         8         •           16         POL         765         SFVYVPSAL         2848         9         •           19         POL         413         SWLSLDVSAFF         2849         11         •           20         BW         334         SWLSLLVPF         2850         9         •           20         BW         392         SWPKFAVPIL         2851         10         •           20         BW         197         SWWTSLNF         2852         8         •	100	20	8	332	RFSWLSLLVPF	2840	Ξ		
19         BW         236         RWMCLRRF         2842         8           19         BW         236         RWMCLRRF         2843         9         *           19         BW         236         RWMCLRRF         2845         11         *           20         POL         167         SFCGSPYSW         2846         9         *           19         NUC         46         SFLPSDF         2848         9         *           16         POL         765         SFVYVPSAL         2848         9         *           19         POL         413         SWLSLDVSAF         2849         11         *           20         BW         334         SWLSLLVPF         2850         9         *           20         BW         197         SWMYSLNF         2852         8         *           20         BW         197         SWMYSLNF         2852         8         *	85	17	젚	577	RWGYSLNF	2841	80		
19         BNV         236         RWMCLRRFI         2843         9         *           19         BNV         236         RWMCLRRFII         2845         11         *           20         POL         167         SFCGSPYSW         2846         9         *           19         NLC         46         SFLPSDF         2847         8         *           16         POL         765         SFVYVPSAL         2848         9         *           19         POL         413         SWLSLDVSAF         2849         11         *           20         BW         334         SWLSLLVPF         2850         9         *           20         BW         197         SWMTSLNF         2851         10         *           20         BW         197         SWMTSLNF         2852         8         *	98	19	AG M	236	RWMCLRRF	2842	80		
19         BNV         236         RWMCLRRFII         2844         10         *           20         POL         167         SFCGSPYSW         2846         9         *           19         NUC         46         SFLPSDF         2847         8         *           16         POL         765         SFVYVPSAL         2848         9         *           19         POL         413         SWLSLDVSAF         2849         11         *           20         BW         334         SWLSLLVPF         2850         9         *           20         BW         197         SWMTSLNF         2851         10         *           20         BW         197         SWMTSLNF         2852         8         *	95	19	AB M	236	RWMCLRRFI	2843	6	•	0.0710
19         BNV         236         RWMCLRRFIIF         2845         11           20         POL         167         SFCGSPYSW         2846         9         *           19         NLC         46         SFLPSDFF         2847         8         *           16         POL         765         SFVYVPSAL         2848         9         *           19         POL         413         SWLSLDVSAFF         2849         11         *           20         BNV         334         SWLSLLVPF         2850         9         *           20         BNV         197         SWMYFAVPNL         2851         10         *           20         BNV         197         SWMYFLNF         2852         8         *	95	19	A M	236	RWMCLRRFII	2844	10	•	1.1000
20         POL         167         SFCGSPYSW         2846         9         *           19         NUC         46         SFLPSDFF         2847         8         *           16         POL         765         SFVYVPSAL         2848         9         *           19         POL         413         SWLSLDVSAAF         2849         11         *           20         BW         334         SWLSLLVPF         2850         9         *           20         BW         197         SWPKFAVPIL         2851         10         *           20         BW         197         SWMTSLNF         2852         8         *	95	19	æ	236	RWMCLRRFIIF	2845	=		
19 NUC 46 SFLPSDFF 2847 8 16 POL 765 SFVYVPSAL 2848 9 19 POL 413 SWLSLDVSAAF 2849 11 20 BW 334 SWLSLLVPF 2850 9 19 POL 392 SWPKFAVPNL 2851 10 20 BW 197 SWWTSLNF 2852 8	100	20	젍	167	SFCGSPYSW	2846	თ	•	0.0710
16 POL 765 SFVYVPSAL 2848 9 19 POL 413 SWLSLDVSAAF 2849 11 20 BW 334 SWLSLLVPF 2850 9 19 POL 392 SWPKFAVPNL 2851 10 20 BW 197 SWWTSLNF 2852 8	98	19	SEC.	.46	SFLPSDFF	2847	80		
19 POL 413 SWLSLDVSAAF 2849 11 20 EM 334 SWLSLLVPF 2850 9 • 19 POL 392 SWPKFAVPNL 2851 10 • 20 EM 197 SWWTSLNF 2852 8	80	16	젍	765	SFVYVPSAL	2848	თ		
20 ENV 334 SWLSLLVPF 2850 9 • • • • • • • • • • • • • • • • • •	95	19	ප්	413	SWLSLDVSAAF	2849	Ξ		
19 POL 392 SWPKFAVPNL 2851 10 • 10 • 197 SWWTSLNF 2852 8	100	20	AG M	334	SWLSLLVPF	2850	6	•	0.3900
20 EW 197 SWWTSLNF	95	19	&	392	SWPKFAVPNL	2851	10	•	5.6000
	000	ć	č	,					

ancy Freq. Protein Position  19	rable XVIII			HBV A24 M	HBV A24 Motif With Binding Information	<u>Information</u>			
5 19 BW 197 5 15 POL 4 5 15 POL 4 6 15 POL 4 6 15 POL 4 7 15 POL 4 7 15 POL 657 6 19 POL 657 6 19 POL 657 7 138 7 131 8 NUC 102 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237 8 19 BW 237		Freq.	Protein	Position	Sequence	SEQ ID NO:	¥ ¥	Filed	A*2401
5 15 POL 4 15 POL 4 15 POL 4 16 POL 4 17 POL 4 18 POL 4 19 POL 657 19 POL 6657 19 POL 6657 19 POL 686 19 POL 686 19 POL 687 19 POL 687 19 POL 686 19 POL 6		19	W <sub>0</sub>	197	SWMTSLNFL	2853	6	•	0.3800
5 15 POL 4 5 15 POL 4 6 15 POL 4 7 15 POL 4 7 1 18 POL 138 7 19 POL 657 7 19 POL 686 7 19 POL 687 7 19 POL 68		18	전	537	SYMDDVVL	2854	80		
5 15 POL 4 5 15 POL 4 6 15 NUC 138 7 15 NUC 138 7 19 POL 657 7 19 POL 686 7 19 POL 687 7 19 POL		15	ಕ	4	SYQHFRKL	2855	80		
5 15 POL 4 5 15 NUC 138 6 15 NUC 138 7 19 POL 657 7 19 POL 686 7 19 POL 687 7 19 PO		15	전	4	SYCHFRKIL	2856	თ		0.0051
5 15 POL 4 5 15 NUC 138 6 19 POL 657 7 19 POL 667 7 19 POL 686 7 19 POL 687 7 19 PO	75	15	ರ	4	SYQHFRKLLL	2857	. 10	•	0.0660
5 15 NUC 138 5 19 POL 657 5 19 POL 657 5 19 POL 667 5 19 POL 686 6 19 POL 886 6 19 POL 886 6 19 POL 886 7 131 7 POL 89 6 19 POL 89 7 131 8 POL 886 7 131 8 POL 886 8 131 8 POL 886 8 131 8 POL 886 8 131 8 POL 887 8 131 8 POL 837 8 131 8 POL 8 P	75	15	ಶ	4	SYQHFRKLLLL	2858			
5 15 NUC 138 5 19 POL 657 5 19 POL 657 5 19 POL 686 6 19 POL 686 6 19 POL 886 6 19 POL 886 6 19 POL 886 7 131 7 POL 897 7 POL	75	15	2	138	TFGRETVL	2859	80		
5 19 POL 657 5 19 POL 657 5 19 POL 686 6 18 X 131 6 18 NUC 102 6 19 BNV 345 5 19 BNV 237 5 19 BNV 237 6 19 BNV 237 6 19 BNV 237 6 19 BNV 237 6 19 BNV 237 6 19 BNV 237 6 11 BNV 237 6 11 BNV 237	7.5	15	2	138	TFGRETVLEYL	2860	=		
5 19 POL 657 5 19 POL 686 6 15 X 131 6 18 NUC 102 6 19 BNV 345 5 19 BNV 237 5 19 BNV 237 6 19 BNV 237 6 19 BNV 237 6 19 BNV 237 6 19 BNV 237 6 11 BNV 237 6 11 BNV 237	95	19	전	657	TFSPTYKAF	2861	თ		0900'0
5 19 POL 686 5 15 X 131 6 18 NUC 102 5 19 BNV 345 5 19 BNV 237 5 19 BNV 237 5 19 BNV 237 5 19 BNV 237 6 17 BNV 237	95	19	절	657	TFSPTYKAFL	2862	01		0.0043
5 15 X 131  0 18 NUC 102  5 19 ENV 345  5 19 ENV 237  5 19 ENV 237  5 19 ENV 237  5 19 ENV 237  5 17 ENV 359	95	19	ಕ್ಷ	989	VFADATPTGW	2863	10	•	0.0180
6 18 NUC 102 5 19 ENV 345 5 19 ENV 237 5 19 ENV 237 6 19 ENV 237 6 19 ENV 237 6 17 ENV 359	7.5	15	×	131	VFVLGGCRHKL.	2864	=		
5 19 ENV 345 5 19 ENV 237 5 19 ENV 237 5 19 ENV 237 5 19 ENV 237 5 17 ENV 359	06	18	SE SE	102	WFHISCLTF	2865	o	•	0.0300
5 19 EW 345 5 19 EW 237 5 19 EW 237 5 19 EW 237 5 17 EW 359	98	19	A B	345	WFVGLSPTVW	2866	10	•	0.0120
5 19 EW 237 5 19 EW 237 5 19 EW 237 5 19 EW 237 5 17 EW 359	95	19	AG	345	WFVGLSPTVML	2867	=		
5 19 EW 237 5 19 EW 237 5 19 EW 237 5 17 EW 359	95	19	A M	237	WMCLRRFI	2868	œ		
5 19 BW 5 19 BW 5 17 BW	95	19	A M	237	WMCLRRFII	2869	თ	•	
5 19 BW 5 17 BW		19	8	237	WMCLRRFIIF	2870	10		0.0013
5 17 ENV		19	A B	237	WMCLRRFIIFL	2871	=		
	85	17	<u>8</u>	359	WMMWWGPSL	2872	10	•	
19 EW	98	19	A.	198	WWTSLNFL	2873	80		

## HBV DR-SUPER MOTIF

Table XIXa

Core SEQ ID NO:	Core	Core Freq.	Core Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position in HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
	FAAPFTOCG	19	95	3021	LLGFAAPFTQCGYPA	. 628	19	95
	FADATPTGW	19	95	3022	COVFADATPTGWGLA	684	16	80
	FAVPNLOSL	19	95	3023	WPKFAVPNLOSLTNL	393	6 :	S 6
	FGHEIMEY	3.	7.5	3024	CLIFGHEIVLEYLVS	136	14	0/
	HGVEPSGSG	5 -	5/2	3025	HHSP-GVEP-SGSGHID	252		30
	ברו יכווים	0 4	D 0	3026	MOLEUN CHIECECO	0 +		60
		9 9	9 6	3028		245	5 4	9 6
	FLFILLG	9 -	80	3020	FIFFFILLCLIFL	243	9 1	08
	FIGHLMO	15	7.5	3030	TSGFLGPLLVLQAGF	168	15	7.5
	FLLTRILTI	16	80	3031	AGFFLLTRILTIPOS	180	16	80
	FLYLLDYO	19	98	3032	CLIFILVILDYQGML	253	19	95
	FPAGGSSSG	15	7.5	3033	GLYFPAGGSSSGTVN	127	Ξ	55
	FPDHOLDPA	18	06	3034	LGFFPDHQLDPAFGA	22	<b>6</b>	45
	<b>FPHCLAFSY</b>	19	95	3035	RRAFPHCLAFSYMDD	527	19	95
	FRKIPMGVG	16	80	3036	ILGFRKIPMGVGLSP	498	13	65
	FRKLPVNRP	16	80	3037	KOCFRKLPVNRPIDW	616	6	45
	FSSAGPCAL	19	95	3038	VCAFSSAGPCALRFT	09	18	06
	FSWLSLLVP	20	100	3039	SVRFSWLSLLVPFVQ	330	16	80
	FTFSPTYKA	19	95	3040	KOAFTFSPTYKAFLC	653	12	09
	FTGLYSSTV	18	06	3041	VGNFTGLYSSTVPVF	99	Ξ	55
	FTSAICSVV	19	95	3042	LAOFTSAICSVVRRA	515	19	95
	FVGLSPTVW	19	92	3043	VQWFVGLSPTVMLSV	343	14	70
	FAGGCRHK	18	06	3044	LKVFVLGGCRHKLVC	129	14	70
	FVOWFVGLS	6	95	3045	LVPFVQWFVGLSPTV	339	6- 9	56
	FVYVPSALN	- 18	06	3046	GTSFVYVPSALNPAD	763	9 :	80
	DWKVCQRI	17	32	3047	NHPIDWKVCQHIVGL	614	9 .	080
	FLFILLC	9 ;	08	3048	RFIIFLECLIF	242	S	75
	IPLEVELDY	D (	ກິດ	3049	LCUFILVICOM 100 TOTOLOGIA	797	D (	n 1
	IGIDINSVAL	9 !	0 0	3050	AKLIGIUNSVVLSHK	(3)	e	ç ç
	IHIAELLAA	<u> </u>	က	3051	PLPIH I AELLAACPA	<u> </u>	٥,	2 1
	IIPLFILL III 21 15	9 ;	28	3052	HAFIIFLECTI	241	နှင့်	92
	ורוכנואר	50	90 6	3053	FLFILLCUFLLVL	246	9 9	08
	LAGIOPY STIPETT	9 C	Q (C)	3054	ANWILLIGI SITVIVES	15.7	0 0	0 se
	PIPSSWAF	2 0	8 5	3056	CTCIPIPSSWAFABE	321	2 ∝	0 4
	IRTPPAYRP	61	95	3057	GVWIRTPPAYRPPNA	123	5	56
	LAACFARSR	17		3058	AELLAACFABSBSGA	717	9	80
	LAFSYMDDV	18	06	3059	PHCLAFSYMDDVVLG	531	18	06
	LAOFTSAIC	19	92	3060	PFLLAGFTSAICSVV	512	19	95
	LCLGWLWGM	17	85	3061	ASKLCLGWLWGMDID	19	17	85
	CCLIFLLY	20	100	3062	ILLICUFLIVILDY	249	. 61	98
	LCLRPVGAE	19	95	3063	RDVLCLRPVGAESRG	13	18	06
	LCQVFADAT	19	. 95	3064	RPGLCQVFADATPTG	089	=	55
	LDSWWTSLN	19	95	3065	POSLDSWWTSLNPLG	192	17	85
	LDTASALYR	17	85	3066	RDLLDTASALYREAL	28	16	80
	LDVSAAFYH	19	95	3067	WLSLDVSAAFYHIPL	425	Ξ	55
	LDYGGMLPV	18	06	3068	LVLLDYQGMLPVCPL	258	18	06
	LEEELPRIA	18	06	3069	AGPLEEELPRLADEG	18	. 13	65
	LFILLIALI	16	08.	3070	IIFLFILLCLIFLL	244	16	80
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Table XIXa

Protein	Core SEQ ID NO:	Core . Sequence	Core Freq.	Core Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position In HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
전	2924	LGAKSVOHL	17	85	3071	DVVLGAKSVQHLESL	541	16	80
ಕ	2925	LGFAAPFTQ	19	95	3072	VGLLGFAAPFTQCGY	626	19	95
<b>ಜ</b>	2926	LGFRKIPMG	19	98	3073	PIILGFRKIPMGVGL	496	13	65
ಕ	2927	LGNLNVSIP	19	95	3074	DLNLGNLNVSIPWTH	40	19	95
<b>&amp;</b>	2928	LGPLLVLOA	19	92	3075	SGFLGPLLVLQAGFF	169	15	7.5
전 :	2929	LHPAAMPHL	50	100	3076	HLPLHPAAMPHLLVG	425	တ	45
<b>2</b> 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	2930	LIFLLVLLD	19	95	3077	LLCUFLLVLLDYGG	251	19	95
덛,	2931	LKLIMPARF	3.	7.5	3078	KRRLKLIMPARFYPN	104	7	35
۶ ۲	2832	LAVINGGC	n •	۲,	3079	EIFLKVFVLGGCKHK	126		65
2 2	2934	LLDTASALY	- <del>-</del>	n 40	3080	SPECACE SAICSV IBDI I DTASAI YREA	16	<u> </u>	9. 4 5. 5.
ಕ್ಷ	2935	LEGCAANWI	16	08	3082	FPWILGCAANWILRG	749	5.	7.5
ğ	2936	LLGFAAPFT	19	95	3083	IVGLLGFAAPFTQCG	625	8-	06
<b>№</b>	2937	LIGWSPOAD	17	85	3084	HGGLLGWSPQAQGIL	09	15	7.5
₽% PM	2938	LLCLFL	20	100	3085	LFILL LCLIFLE VL	247	16	80
SE SE	2939	LLSFLPSDF	19	98	3086	SVELLSFLPSDFFPS	41	Ξ	55
<u>ಕ</u>	2940	LLSLGIHLIN	19	92	3087	TNFLLSLGIHLNPNK	260	15	7.5
ೱ	2941	LLSSNLSWL	18	06	3088	LTNLLSSNLSWLSLD	404	18	06
<b>8</b>	2942	LLTRILTIP	16	80	3089	GFFLLTRILTIPQSL	181	16	80
<b>&amp;</b>	2943	LLVLOAGFF	19	92	3090	LGPLLVLQAGFFLLT	172	18	06
& 6	2944	LLVPFVQWF	20	100	3091	WLSLLVPFVQWFVGL	335	19	95
2	2945	LLWFHISCL	<del>-</del>	06	3092	IROLLWFHISCLTFG	126	13	65
	2946	LMPLYACIO	19	92	3093	YPALMPLYACIOSKO	640	Ξ	55
ಕ :	2947	INICALINAS	19	92	3094	AEDLNLGNLNVSIPW	38	19	95
ಕ :	2948	LNPNKTKRW	5	7.5	3095	GIHLNPNKTKRWGYS	267	15	7.5
ಶ :	2949	UNRRVAEDL	17	82	3096	DEGLNRRVAEDLNLG	30	12	09
g :	2950	LNVSIPWTH	6 9	95	3097	LGNLNVSIPWTHKVG	43	6 :	95
2 2	2951	LPETTWAR	19	95	3098	LSTLPETTWRRAGA	169	9 .	80
£ 8	2822	CHITCHW	07,	00.5	3099	LPLLPIFFCLWVYIZ	3/6		59
<b>4</b> 8	2953	LPIHTAELL		S 0	3100	VAPLPIHTAELLAAC	709	o !	45
<b>로</b> 8	2954	PVNHPIDW OCCUPATION	9 9	0.60	3101	FHKLPVNHPIDWKVC	809	5.	75
ಕ,	2955	CHANKE	æ (	0 0	3102	CWWLQFHNSKPCSDY	312	0,	20
< >	2926	CHGLPVCAF	-		3103	HLSCHGLPVCAPSSA	55	90 0	06
<u> </u>	7827	LAPVGAESH LOOM CAIC	D 0	5 6	3104	VLCLHPVGAESHGHP	ر د	20 G	) 5
3 2	2050	I BREIIE F	- <del>-</del>	0° C	200	WAACI BREIEF EILI	766	- + - 4	3 6
2	2960	LSALPSOFF	0 0	o 46	3107	VELL SELPSOFFPS	42	2 9	50
್ದ ಜ್ಞ	2961	LSLDVSAAF	19	9.5	3108	LSWLSLDVSAAFYHI	423	: =	55
<b>₩</b>	2962	LSLLVPFVQ	20	100	3109	FSWLSLLVPFVQWFV '	333	19	95
×	2963	LSLRGLPVC	19	9.2	3110	GAHLSLRGLPVCAFS	20	18	90
젙	2964	LSPFLLAOF	19	95	3111	GVGLSPFLLAGFTSA	207	16	80
	2965	LSRKYTSFP	17	85	3112	SVVLSRKYTSFPWLL	739	17	85
젍	2966	LSSNLSWLS	18	06	3113	TNLLSSNLSWLSLDV	405	18	06
₩.	2967	LSVPNPLGF	15	7.5	3114	GTNLSVPNPLGFFPD	13	14	70
ಶ :	2968	LSWLSLDVS	20	100	3115	SSNLSWLSLDVSAAF	409	17	85
26	2969	LTIPOSLDS	8 :	06	3116	TRILTIPOSLDSWWT	186	- 15	7.5
<b>z</b> 2	2970	LTNLLSSNL	<del>6</del> (	06	3117	LOSETNILLSSNLSWL	401	8 :	06
<b>&amp;</b> 3	2971	LTRILTIPO	16	08	3118	FFLLTRILTIPOSLD	182	- 15	7.5
호 :	2972	LVDKNPHNT	20	100	3119	GVFLVDKNPHNTTES	372	= :	55
3	2973	LVSFGVWIR	18	O -	3120	LEYLVSFGVWIRTPP	. 145	4	70

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Table XIXa

Protein	Core SEQ ID NO:	Core Sequence	Core Freq.	Core Conservancy (%)	Exemplary SEQ ID NO:	Exemplary Sequence	Position In HBV Poly-Protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ಕ	2974	LWDFSQFS	20	100	3121	ESPLWDFSQFSPGN	374	6	45
32	2975	LWFHISCLT	17	85	3122	ROLLWFHISCLTFGR	86	17	85
3	2976	LWGMDIDPY	17	85	3123	LGWLWGMDIDPYKEF	24	17	85
점	2977	LWKAGILYK	20	100	3124	LHTLWKAGILYKRET	148	18	06
3	2978	LYREALESP	17	85	3125	ASALYREALESPEHC	34	17	85
	2979	LYSHPIILG	16	80	3126	KLHLYSHPIILGFRK	489	16	80
젍	2980	MDDVVLGAK	6	06	3127	FSYMDDVVLGAKSVQ	536	18	06
젍	2981	MGVGLSPFL	16	80	3128	KIPMGVGLSPFLLAQ	503	16	80
젙	2982	MPHILVGSS	17	85	3129	PAAMPHLLVGSSGLS	430	80	40
PN V	2983	MOWNSTITH	16	80	3130	POAMOWNSTTFHOTL	106	83	40
×	2984	MSTTDLEAY	15	75	3131	LSAMSTTDLEAYFKD	100	6	45
8	2985	MWYWGPSLY	17	85	3132	IWMMWYWGPSLYNIL	369	6	45
×	2986	VCAFSSAGP	19	95	3133	GLPVCAFSSAGPCAL	57	18	06
젙	2987	VCORIVGIL	17	85	3134	DWKVCQRIVGLLGFA	618	17	85
ರ್ಷ	2988	VFADATPTG	19	95	3135	LCQVFADATPTGWGL	683	19	96
8	2989	VGLSPTVML	19	95	3136	QWFVGLSPTVWLSVI	344	14	70
젒	2990	VGPLTVNEK	17	85	3137	QQYVGPLTVNEKRRL	93	æ	40
젒	2991	VHFASPLHV	16	80	3138	PDRVHFASPLHVAWR	816	12	09
×	2992	VLCLRPVGA	19	95	3139	ARDVLCLRPVGAESR	12	14	7.0
젒	2993	VLGAKSVQH	19	98	3140	DDVVLGAKSVQHLES	540	16	80
×	2994	VLHKRTLGL.	17	85	3141	LPKVLHKRTLGLSAM	88	=	55
젒	2995	VPNLOSLTN	19	9.2	3142	KFAVPNLOSLTNLLS	395	19	95
3	2996	VOASKLCLG	16	80	3143	CPTVQASKLCLGWLW	14	15	7.5
<b>₩</b>	2997	VRFSWLSLL	16	80	3144	WASVRFSWLSLLVPF	328	13	65
ೱ	2998	VRRAFPHCL	19	95	3145	CSWARAFPHCLAFS	523	19	95
정	2999	VSIPWTHKV	20	100	3146	NLNVSIPWTHKVGNF	45	19	92
3	3000	VWIRTPPAY	19	98	3147	SFGVWIRTPPAYRPP	121	18	06
절	3001	VYVPSALNP	18	06	3148	TSFVYVPSALNPADD	764	16	80
SEC SEC	3002	WFHISCLTF	18	06	3149	<b>CALLWFHISCLTFGRE</b>	66	17	85
<b>8</b>	3003	WFVGLSPTV	19	95	3150	FVQWFVGLSPTVMLS	342	19	92
전	3004	WILRGTSFV	16	80	3151	AANWILRGTSFVYVP	756	14	70
2	3005	WIRTPPAYR	19	96	3152	FGVWIRTPPAYRPPN	122	19	95
ರ್ಷ	3006	WKAGILYKR	20	100	3153	HTLWKAGILYKRETT	149	18	06
ಶ	3007	WLLGCAANW	16	80	3154	SFPWLLGCAANWILR	748	15	7.5
ರ್ಷ	3008	WLSLDVSAA	19	95	3155	NLSWLSLDVSAAFYH	411	17	85
<b>%</b>	3009	WLSLLVPFV	20	100	3156	RESMLSLLVPFVQWF	332	20	100
ಶ	3010	WPKFAVPNL	19	95	3157	RVSWPKFAVPNLQSL	390	Ξ	55
	3011	YMDDVVLGA	18	06	3158	AFSYMDDVVLGAKSV	535	18	06
ಕ್ಷ	3012	YPALMPLYA	19	95	3159	<b>QCGYPALMPLYACIQ</b>	637	19	95
<u>₹</u>	3013	YOGMLPVCP	81	0.6	3160	LLDYQGMLPVCPLIP	260	10	20
2	3014	YRPPNAPIL	20	100	3161	PPAYRPPNAPILSTL	129	19	95
&	3015	YRWMCLRRF	19	95	3162	CPGYRWMCLRRFIIF	232	19	95
ಶ	3016	YSHPIILGF	16	80	3163	LHLYSHPIILGFRKI	490	16	80
ಶ	3017	YSLNFMGYV	15	7.5	3164	RWGYSLNFMGYVIGS	588	=	55
<u>ಕ</u>	3018	YVPSALNPA	18	06	3165	SFVYVPSALNPADDP	765	16	80
2	3019	<b>FFCLWYYIZ</b>	20				382		
8	3020	MGTNLSVPN	15				12		

## HBV DR-SUPER MOTIF With Binding Data

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Drw53	0.0180				0.0150		0.0190	6	2.6000				•		0.1600			0.0010						
DR9			1.3000		0.0250	0.5400	0.0880	1	0.3400							0.0450		0.0590						
DR8W2			0.2600		0.0580	0.1200	0.0150	0	0.6600							0.5300		0.0580						
DR7	0.0008	0.0018	3.1000	0.0017	0.0200	0.3300	0.0280		0.2700		0.0044	-0.0003			0.0005	0.2200		0.0770	0.0047		0.0770		0.0011	
DR6w19			0.3700		0.0043	0.0200	0.0010	0	0.0001			•				-0.0004		0.0800						
DR5w12			0.0700		0.0013	0.0024	0.0091	0	0.0001							0.0140		0.0016						
· DR5w11	0.0002	٠	3.6000	0.0010	0.0130	0.2400	0.0076	000	0.3800		0.0017			;	-0.0002	0.4800		0.0120 -0.0002	0.0018					
DR4w15	0.2800		0.1500		0.8500	0.2200	0.0280	,	0.4100							0.5700		0.1200						
DR4w4	0.0023	0.0041	5.3000	-0.0009	0.0023	1.1000	0.0150		0.3800		0.0230	0.0490			-0.0007	3.4000		0.0800	0.0320		0.0092		0.0013	
DR3			0.0040		-0.0006	0.0090	-0.0009	0	0.0003							0.0120		-0.0013					0.0022	
DR2w2β2	0.0013		0.0190	0.0010	0.0210	0.1400	0.1500	9	0.0140		0900'0				0.0009	7.2000		0.0042	6900.0					
DR2w281			0.0420		0.0022	0.2400	0.0065	0000	0.0140							0.0420	į	0.0270						
OR1	0.0007	0.0005	4.6000	0.0010	0.2100	0.5300	0.0120	0	0.3500		0.0016	0.0046			0.0009	0.3700		0.1800	0.0026	٠	0.0001		0.0034	٠
Exemplary Sequence	LLGFAAPFTQCGYPA CQVFADATPTGWGLA WPKFAVPNLQSLTNL CLTFGRETVLEYUS RRSFGVEPSGSGHID	LLWFHISCL TFGRET MOLFHLCLIFLS FIFFILLCLIFLV FIFFILLCLIFL TSGEI CELI VI OAGE	AGFFLTRILTIPQS CLIFLLVLDYQGML GLYFPAGGSSSGTVN LGFFPDHQLDPAFGA	RRAFPHCLAFSYMDD ILGFRKIPMGVGLSP	KQCFRKLPVNRPIDW VCAFSSAGPCALRFT	SVRFSWLSLLVPFVQ KQAFTFSPTYKAFLC VGNFTGI YSSTVPVF	LAQFTSAICSVVRRA VQWFVGLSPTVWLSV	LKVFVLGGCRHKLVC	GTSFVYVPSALNPAD	NRPIDWKVCQRIVGL RFIIFLFILLLCLIF	LCLIFLLVLLDYQGM	PLPIHTAELLAACFA	RRFIIFLFILLCLI FLFILLCLIFLLVL	ANWILRGTSFVYVPS	CTCIPIPSSWAFARF	GVWIRTPPAYRPPNA AELLAACFARSRSGA	<b>PHCLAFSYMDDVVLG</b>	PFLLAQF I SAICSVV ASKLCLGWLWGMDID	ILLLCLIFLLVLLDY	RPGLCQVFADATPTG	POSLDSWWTSLNFLG RDLLDTASALYREAL	WLSLDVSAAFYHIPL	LVLLDYQGMLPVCPL AGPLEEELPRLADEG	ון רו ורדר כריי דר
SEO ID NO:	3021 3022 3023 3024 3025	3026 3027 3028 3029	3031 3032 3033 3034	3035 3036	3037	3040 3040	3042 3042 3043	3044	3046	3047 3048	3049	3051 3051	3052 3053	3054	3025 3056	3057	3059	3060 3061	3062	3064	3065 3066	3067	3068 3069	3
Core Sequence	FAAPFTQCG FADATPTGW FAVPNLQSL FGRETVLEY	FHISCLTFG FHLCLIISC FILLCLIF FLFILLCL	FLLTRILTI FLLVLLDYQ FPAGGSSSG FPDHQLDPA	FPHCLAFSY FRKIPMGVG	FRKLPVNRP FSSAGPCAL	F1FSPTYKA F1FSPTYKA	FTSAICSVV	FVLGGCRHK	FVYVPSALN	IDWKVCQRI IFLFILLLC	IFLLVLLDY ICTONSON!	INTAELLAA	IIFLFILL ILLCLIFL	ILRGTSFVY	ILSTLPETT IPIPSSWAF	IRTPPAYRP LAACFARSR	LAFSYMDDV	LCLGWLWGM	LCLIFLLVL	LCQVFADAT	LDSWWTSLN LDTASALYR	LDVSAAFYH	LDYQGMLPV LEEELPRLA	נו וינו אינ
SEQ ID NO:	2874 2875 2876 2877	2879 2880 2881 2882 2883	2884 2885 2886 2887	2888 2889	2890 2891	2892 2893 2894	2895 2896	2897	2898	2900 2901	2802	2803 2804	2905 2906	2907	2308 2303	2910 2911	2912	2913 2914	2915	2917	2918 2919	2920	2921 2922 2923	7707

Table XIXB				HBV [	HBV DR-SUPER MOTIF With Binding Data	MOIT	With B	inding	ata					
Core	SEQ ID	Exemplary Sequence	8	DR2w2B1	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8w2 DR9	DRw53
LGAKSVOHL LGFAAPFTO		DVVLGAKSVQHLESL VGLLGFAAPFTQCGY	0.0470	0.3100	0.0008	•	-0.0014		-0.0004	·	-0.0001	0.0014	0.5700	
LGNLNVSIP	3074	PILICE FINIT PROPERTY OF THE P	0.0038				0.0240					0.0010		
LGPLLVLOA	3076	SCILCEPLY LOAGEF HLPLHPAAMPHLLVG												
LIFLLVILD	3077	LLCLIFLLVLLDYOG KRRLKLIMPARFYPN												
LKVFNLGGC	3079	EIRLKVF/ALGGCRHK												
LLAOFTSAI	3080 3081	SPFLLAQFTSAICSV IRDLLDTASALYREA	0.1200	0.0200	0.0085	-0.0013	0.0740	0.0190	-0.0002	-0.0013 0.0540	0.0540	0.0330	0.0014 0.0380	0.2000
LLGCAANWI		<b>FPWLLGCAANWILRG</b>												
LIGEAAPFT	3083	IVGLLGFAAPFTOCG HGGLLGWSPOAOGII	0.0200		-0.0005		-0.0007		-0.0002			0.000		0.0067
LLCIFL		LFILLCLIFLEVIL												
LISFLPSDF	3086	SVELLSFLPSDFFPS												
LESTGIHLN	3087	TNFLLSLGIHLNPNK	3.5000	0.0410	0.1200		0.0220	0.0360	0.0053		0.0160		0.0032 0.3800	
LLTRILTIP	3089	GFFLLTRILTIPOSL	0.0010	0.0150	0.0083		3.1000	0.4500	2.3000		0.0780	3.5000	1.6000 0.5500	0.0200
LL/LOAGFF	3090	LGPLLVLOAGFFLLT												
LLVPFVQWF	3091	WLSLLVPFVQWFVGL												
I MPI YACIO	3063	YPAI MPI YACIOSKO	0.2400				0 00 14							
INIGNIANS	3094	AEDLNLGNLNVSIPW	0.0001		-0.0005		-0.0007		-0.0002			-0.0003		0.0170
LNPNKTKRW	_	GIHLNPNKTKRWGYS												
LNRRVAEDL	3096	DEGLINARIVAEDLNLG												
LPETTWAR	3098	LSTLPETTWARAGA												
LPIFFCLWV	3099	LPLLPIFFCLWVYIZ												
LPIHTAELL	3100	VAPLPIHTAELLAAC												
LOFFNSKPC		CWMLOFFINSKPCSDY												
LAGLPVCAF		HLSLRGLPVCAFSSA	1.3000				0.0028					0.0130		
LHPVGAESH I BOAII CWG	3104	VICHEVGAESHGRP												
LARFIIFLE		WMCLRRFIIFLFILL												
LSFLPSDFF		VELLSFLPSDFFPSI												
LSLDVSAAF		LSWLSLDVSAAFYHI												
LSLIVPFVO	3109	FSWLSLLVPFVOWFV	9		0				0					
LSPFLLAGF		GVGLSPFLLAOFTSA	0.7860		0.0042	-0.0041	1.00.0		0.0025			0.0077		0.0150
LSRKYTSFP	_	SVVLSRKYTSFPWLL	0.0005		0.0057	0.2100	-0.0016		0.5300			0.0130		
LSSNLSWLS		TNLLSSNLSWLSLDV	0.0016		-0.0005		0.1300		0.0006			0.0019		0.0410
LSVPNPLGF		GTNLSVPNPLGFFPD					,							
LEWISLDVS	3116	SSNLSWLSLDVSAAF TRILTIPOSLDSWWT	0.1400	0.0030	-0.0005	1.5000	0.2700		0.0046	0.0180	0.1000	0.0039	0.0460 0.0110	6.2000
LTNLLSSNL		LOSLTNLLSSNLSWL	2.5000	0.4400	0.0200	-0.0013	4.8000	0.8100	0.0680	0.7500	0.0260	0.1500	0.0880 0.1100	
LTRILTIPO		FFLLTRILTIPOSLD												
LVDKNPHNT	3119	GVFLVDKNPHNTTES												
Lvardywin		רבוראאוטוגג												

tble XIXB					HBV D	HBV DR-SUPER MOTIF With Binding Data	NOTIF	With B	inding D	ata				•	
Core SEQ ID NO:	Core Sequence	SEO ID NO:	Exemplary Sequence	DRI	DR2w281	DR2w282	D <del>.</del> 33	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8w2 DR9	DRw53
2974	LWDFSQFS	3121	ESPLWDFSOFSRGN ROLLWFHISCLTFGR	0.0007	0.0074	0.0010	2.6000	0.0140		-0.0004		0.0040	-0.0014	0.0029	0.0096
2976	LWGMDIDPY WKAGII YK	3123	LGWLWGMDIDPYKEF	0.0004		9000'0	0.0200	0.0280		-0.0002			0.0004		0.0430
2978	LYREALESP	3125	ASALYREALESPEHC												
2979	MDDWLGAK	3126	KLHLYSHPIILGFRK FSYMDDVVI GAKSVO												
2981	MGVGLSPFL	3128	KIPMGVGLSPFLLAG										•		
2982	MPHILVGSS	3129	PAAMPHILVGSSGLS	0									0		
2983	MSTTDLEAY	3131	LSAMSTTDLEAYFKD	2100.0				0.0300					0.1200		
2985	MWYWGPSLY	3132	IWMMWWGPSLYNIL												
2986	VCAFSSAGP	3133	GLPVCAFSSAGPCAL	0 0 1 2 0		9000		0000		0036			9		00100
2988	VFADATPTG	3135	LCOVFADATPTGWGL	0.0020		0.0020		0.9600		0.5300			0.0013		0.0
2989	VGLSPTVML	3136	<b>CWFVGLSPTVMLSVI</b>												
2990	VGPLTVNEK	3137	COVYGPLTVNEKRRL												
2991	VHFASPLHV	3138	PORVHFASPLHVAWR	0.0510	0.0290	0.0008		0.0008	0.0054	0.0008		0.0190	0.0810	0.0035 0.2400	_
2992	VLCLRPVGA VI GAKSVOH	3139	ARDVLCLRPVGAESH												
2994	VUHKRILGL	3141	LPKVLHKRTLGLSAM												
2995	VPNLOSLTN	3142	KFAVPNLOSLTNLLS	0.0180	0.0005	-0.0003		0.1300		0.0043		0.0088	-0.0003	0.0056	<b></b>
2996	VOASKLCLG	3143	CPTVQASKLCLGWLW												
2997	VRFSWLSLL	3144	WASVRESWLSLLVPF	0	****	0,00	6	9 60 0	6			06.40	0000		
9667	VSIPWTHKV	3145	NI NVSIPWTHKVGNE	0.00	0.1024	-0.0005	0.0032	0.0016	-0.0022	0.000	-0.00	0.0340	0.0390	0.0230 1.2000	0.0460
3000	VWIRTPPAY	3147	SFGVWIRTPPAYRPP	0.0094	0.0110	0.4300	-0.0009	0.0780	0.0630	0.0260	0.0071	0.0002	0.0240	0.2500 0.0800	
3001	VYVPSALNP	3148	TSFVYVPSALNPADD												
3002	WFHISCLTF	3149	OLLWFHISCLTFGRE												
3003	WEVGLSPIV	3151	AANWILAGTSFVYVP	0.4700	0.0035	0.0160	0.0013	0.0130	0.0250	0.0072	0.0021	0.0190	0.0690	0.2500 0.2700	0.0044
3005	WIRTPPAYR	3152	<b>FGVWIRTPPAYRPPN</b>												
3006	WKAGILYKR	3153	HTLWKAGILYKRETT												
3008	WLSLDVSAA	3155	NLSWLSLDVSAAFYH	0.1400	0.0003	-0.0005	1.3000	0.2900		0.0033	0.0022	0.0330	0.0041	0.0150 0.0620	0 5.4000
3009	WLSLLVPFV	3156	RFSWLSLLVPFVOWF	0.0430		0.000		-0.0007		0.0002			0.0005		0.0031
3010	WPKFAVPNL	3157	RVSWPKFAVPNLOSL					0							
3011	YMDDVVLGA YPALMPI VA	3158	AFSYMDDVVLGAKSV	0.0027		-0.0005	0.0130	2.9000		0.0006			-0.0003		-0.0005
3012	YOGMLPVCP	3160	LLDYOGMLPVCPLIP	70007		9.00		0.00		0.0023			0.000		
3014	YRPPNAPIL	3161	PPAYRPPNAPILSTL	0.0056		-0.0005		0.0038		0.0022			0.0024		0.0015
3015 3016	YSHPILGF	3162	CHGYSHPIILGFRKI	0.0220	0.0340	0.0400	0.0040	0.6800	0.1600	0.0410	0.0310	0.0002	0.0006	0.0610 0.0490	
3017	YSLNFMGYV	3164	<b>RWGYSLNFMGYVIGS</b>												
3018	YVPSALNPA	3165	SFVYVPSALNPADDP												
3020	MGTNLSVPN														

Table XIXB

	10	PLGFFPDHOLDPAFG	3181	\$6	19	FFPDHOLDP	3166
Exemplar	Position In Poly-Protein	Exemplary Sequence	Exemplary SEQ ID NO:	Core Conservancy (%)	Core Freq.	Core Sequence	Core SEO ID NO:
		otif	HBV DR-3A Motil	HB			

Table XXa

ance %)															
Exemplary Sequence Conservancy (%)	95	75	75	100	80	06	100	95	100	85	88	100	95	95	06
Exemplary Sequence Frequency	6	14	9	11	13	13	20	-11	6	17	6	17	19	18	18
Position In Poly-Protein	10	136	241	360	731	18	120	412	374	34	27	34	683	256	535
Exemplary Sequence	PLGFFPDHOLDPAFG	CLTFGRETVLEYLVS	PRSFGVEPSGSGHID	GGVFLVDKNPHNTTE	AKLIGTDNSVVLSRK	AGPLEEELPRLADEG	TKYLPLDKGIKPYYP	LSWLSLDVSAAFYHI	ESPLWDFSQFSPGN	ASALYREALESPEHC	LWGMDIDPYKEFGAS	NRRVAEDLNLGNLNV	LCQVFADATPTGWGL	FLLVLLDYGGMLPVC	<b>AFSYMDDVVLGAKSV</b>
Exemplary SEQ ID NO:	3181	3182	3183	3184	3185	3186	3187	3188	3189	3190	3191	3192	3193	3194	3195
Core Conservancy (%)	95	75	7.5	100	80	06	100	95	100	98	82	100	\$6	98	06
Core Freq.	19	15	15	50	16	18	50	19	50	17	17	20	91	19	18
Core Sequence	FFDHOLDP	FGRETMEY	FGVEPSGSG	FLVDKNPHN	IGTDNSWL	LEEELPRIA	LPLDKGIKP	LSLDVSAAF	LWDFSOFS	LYREALESP	MOIDPYREF	VAEDLNLGN	VFADATPTG	VLLDYOGML	YMDDVVLGA
Core SEO ID NO:	3166	3167	3168	3169	3170	3171	3172	3173	3174	3175	3176	3177	3178	3179	3180
Protein	ENA	NC NC	젛	젗	젍	ర్డ	ğ	ర్జ	절	3	3	<b>&amp;</b>	ర్జ	EN	ğ

## HCV DR 3A Motif

DRW53													-0.0005
OR9													
DR8W2							0.0029						
DR7							-0.0014				0.0013		0.0003
DR6w19							0.4000						•
DR5w12													
DR5w11	,						-0.0004						90000
DR4w15													
DR4w4											0.9600		2.9000
DR3		0.0790		0.0022	-0.0017		2.6000			0.1400		0.0170	0.0130
R2w2B2							-0.0010						0.0005
DR2w281 DR2w282							0.0074						•
DR1							0.0007				0.0020		0.0027
Exemplary Sequence	PLGFFPOHOLDPAFG CLTFGRETVLEYLYS	RRSFGVEPSGSGHID GGVFLVDKNPHINTTE	AKLIGTDNSVVLSRK	AGPLEEELPRLADEG	TKYLPLDKGIKPYYP	LSWLSLDVSAAFYHI	ESPLWDFSOFSPGN	ASALYREALESPEHC	LWGMDIDPYXEFGAS	NRRVAEDLNLGNLNV	LCOVFADATPTGWGL	FLLVLLDYOGMLPVC	AFSYMDDVVLGAKSV
SEQ ID NO:	3181	3183	3185	3186	3187	3188	3189	3190	3191	3192	3193	3194	3195
Core	FFPOHOLDP FGRETNLEY	FGVEPSGSG FLVDKNPHN	IGTDNSVVL	LEEELPRLA	PLDKGIKP	LSLDVSAAF	LVVDFSQFS	LYREALESP	MOIDPYNGF	VAEDLNLGN	VFADATPTG	VLLDYOGML	YMDDVVLGA
Core SEQ ID NO:	3166 3167	3168 3169	3170	3171	3172	3173	3174	3175	3176	3177	3178	3179	3180

Table XXb

Exemplary Sequence	90.00	55.00	100.00	90.00	35.00	85.00
Exemplary Sequence Frequency	18	-11	20	12	7	11
Position In HBV Poly-Protein	48	655	47	96	. 61	737
Exemplary Sequence	DHGAHLSLRGLPVCA	AFTFSPTYKAFLCKQ	NVSIPWTHKVGNFTG	VGPLTVNEKRRLKL	LPPVGAESRGPPVSG	DNSVVLSRKYTSFPW
SEQ ID NO:	3202	3203	3204	3205	3206	3207
Conservancy (%)	06	. 95	100	85	95	06
Core Freq.	18	91	20	17	19	18
Core Sequence	AHLSLPGLP	FSPTYKAFL	IPWTHKVGN	LTVNEKARL	VGAESHGRP	WLSRKYTS
Core SEQ ID NO:	3196	3197	3198	3199	3200	3201
Protein	×	ಕ	절	절	×	절

## HBV DR-3B Motif With Binding Information

Table XXd

	•
DRw53	
- 84 - 84	
DR8w2	0.0092
0R7	-0.0014
DR6w19	0.0009
DR5w12	
DR5w11	0.0030
DR4w15	·
DR4w4	
DR3	0.0035 2.2000 -0.0017
DR2w2ß2	0.0047
DR2w261	0.0022
DR1	0.0006
Exemplary Sequence	DHGAHLSHGLPVCA AFTESPTWAFLCKO NVSIPWTWCNGHFG VGPLTVNEGRRIKU LPPVCAESRGPVSG DNSVVLSHKYTSFPW
SEO ID NO:	3202 3203 3204 3205 3205 3206
Core Sequence	AHLSLAGLP FSPTYKAFL IPWTHKYGN LTYNEKAFL VGAESPGPP VYLSRKYTS
Core SEO ID NO:	3196 3197 3198 3199 3200 3201

TABLE XXI. Population coverage with combined HLA Supertypes

PHENOTYPIC FREQUENCY Caucasian North Hispanic Japanese Chinese Average **HLA-SUPERTYPES** American Black a. Individual Supertypes A2 45.8 39.0 42.4 45.9 43.0 43.2 **A3** 37.5 42.1 45.8 43.1 52.7 44.2 **B**7 38.6 52.7 48.8 35.5 47.1 44.7 A1 47.1 16.1 21.8 14.7 26.3 25.2 A24 23.9 38.9 58.6 40.1 38.3 40.0 B44 43.0 21.2 42.9 39.1 39.0 37.0 **B27** 28.4 26.1 13.3 13.9 35.3 23.4 B62 12.6 4.8 25.4 36.5 11.1 18.1 B58 10.0 25.1 1.6 9.0 5.9 10.3 b. Combined Supertypes 83.0 A2, A3, B7 86.1 87.5 88.4 86.3 86.2 98.1 A2, A3, B7, A24, B44, A1 99.5 100.0 99.5 99.4 99.3 A2, A3, B7, A24, B44, A1, 99.9 99.6 100.0 99.8 99.9 99.8 B27, B62, B58

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Table XXII	XII			HB	HBV ANALOGS					
A A	Sequence	Fixed Nomen.	A 1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	. 1° Anchor Fixer	Analog	SEQ ID NO:
10	CILLICLIFL		z	>	z	z	z	2	¥	3208
6	RMTGGVFLV	VM2.V9	z	>	z	z	Z	-	∢	3209
6	LMPFVQWFV	VM2.V9	z	>	z	z	z	-	∢	3210
6	RLTGGVRLV	VL2.V9	z	>	z	z	z	-	< <	3211
6	GLCQVFADV	L2.AV9	z	>	z	z	z	-	⋖	3212
6	WLLRGTSFV	112.V9	z	>	z	z	z	-	∢	3213
თ	NEGNENVSV	L2.IV9	z	>-	z	z	z	-	∢	3214
6	YLPSALNPV	VL2.AV9	z	>	z	z	z	-	∢	3215
6	GLWIRTPPV	VL2.AV9	z:	>	z	z	z	-	∢	3216
<b>о</b>	RLSWPKFAV	VL2.V9	Z:	>	z	z	z	-	∢	3217
<b>o</b>	ILGLLGFAV	VL2.AV9	z:	>	z	z	z	-	∢	3218
တ	RMLTIPOSV	IM2.LV9	z	>	z	z	z	-	∢	3219
<b>6</b>	SLDSWMTSV	L2.LV9	Z:	>	z	z	z	-	∢	3220
0	FMLLCLIFL	IM2.L10	z	>	z	>	z	-	∢	3221
9	LMLQAGFFLV	VM2.LV	z	>	z	z	z	-	∢	3222
0	SMLSPFLPLV	IM2.LV1	z	>	Z	z	z	-	∢	3223
9	LMLLDYQGMV	VM2.LV	z	>-	z	z	Z	-	∢	3224
10	FLGLSPTVWV	VL2.LV1	z	>	z	z	z	-	∢	3225
œ	FPAAMPHL		z	z	z	z	>-		∢	3226
ω	HPFAMPHL		Z:	z	z	z	>		∢	3227
<b>œ</b>	HPAAMPHI		z	z	z	z	>		∢	3228
ω .	FMFSPTYK		Z:	z	>-	z	Z		∢	3229
∞ '	FVFSPTYK		z	z	>	z	Z ·		∢	3230
<b>o</b>	FLLTRILTV	L2.1V9	z	>	z	z	z	-	∢	3231
<b>o</b>	ALMPLYACV	L2.IV9	Z :	>	z	z	z	-	4	3232
<b>o</b>	LLAGFTSAV	L2.1V9	z :	<b>&gt;</b> -	z	z	z	-	∢	3233
<b>o</b> (	L PFVQWFV	VL2.V9	z	>-	z	z	z	-	∢	3234
<b>э</b> (	FLLAGFTSV	L2.AV9	z	>	Z	Z	Z	-	∢	3235
n o	KLTSHPV KLEI VSHBI	LZ.1V9	z 2	<b>&gt;</b> :	2 2	zz	2 2	- ;	∢ •	3236
n 0	I SSNI SIAM	12170	zz	->	2 2	Z	2 2	2 -	∢ ·	7525
, σ	E STORES	12 1 70	: z	- >	2 2	2 2	2 2	<b>- ,</b>	∢ •	9000
, a	MAMANAGEN	MOLVO	z	- >	2 2	2 2	2 3	- •	∢ ·	2000
, ,	W OAGED V	12170	. <u>.</u> z	- >	2 2	2 2	2 2	- ,	⋖ ·	3240
ם מ		12170	: z	<b>-</b> >	2 2	2 2	2 2	- ,	⋖ •	3241
		L2.LV3	2 2	≻ ;	Z 2	2 2	2 2	- :	⋖ •	3242
n a	VI DVOGW	13170	. 2	<b>- &gt;</b>	2 2	2 2	2 2	2 -	∢ •	2443
o	YMEDIVI GA	2	: 2	- >	2 2	2 2	2 2	- 2	∢ •	3244
		0// 6/1	: 2	- >	2 2	2 2	2 3	2,	∢ '	3243
n 0	EPA AMPHI I	LZ.AV3	zz	<b>≻</b> 2	2 2	zz	<b>z</b> >	_	∢ •	3246
, ,	LOGIANDLI	•	: 2	2 2	2 2	2 2	- ;		∢	7470
0 0			2 2	z	2 2	2 2	<b>-</b> ;		∢	3248
מ	חראאויחבו		<b>=</b>	z	z	z	<b>&gt;</b>		¥	3249

Table XXII	IJ			HBV	ANALOGS					
A A	Sequence	Fixed Nomen.	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	. 1° Anchor Fixer	Analog	SEQ ID NO:
6	FPVCAFSSA		z	2	z	z	<b>&gt;</b>		ď	3250
<b>o</b>	LPFCAFSSA		z	: <b>z</b>	z	z	<b>&gt;</b>		< ∢	3251
6	LPVCAFSSI		z	z	z	z	<b>&gt;</b>		: ∢	3252
თ	FPALMPLYA		z	z	z	z	>		. ∢	3253
თ	YPFLMPLYA		z	z	z	z	>-		∢	3254
6	YPALMPLYI		z	z	z	z	>-		⋖	3255
თ	FPSRGRLGL		z	z	Z	z	>		∢	3256
6	DPFFGRLGL		z	z	z	z	>		∢	3257
6	DPSRGRLGI .		z	z	z	z	>		∢	3258
თ	SMICSVVRR		z	z	>	z	z		∢	3259
6	SVICSVVRR		z	z	>-	z	z		∢	3260
თ	KVGNFTGLK		z	z	>-	z	z		∢	3261
6			z	z	. 🖈	z	z		∢	3262
6	WFFSQFSR		z	z	>	z	z		∢	3263
6	SVNRPIDWK		Z	z	>-	z	z		4	3264
6	TLWKAGILK		z	z	>-	z	z		∢	3265
6	TLWKAGILR		z	ž	>-	z	z		4	3266
6	TMWKAGILY		<b>&gt;</b> :	z	>-	z	z		∢	3267
6	TVWKAGILY		Z :	Z	>	z	z		4	3268
6	RMYLHTLWK	•	Z:	z	>-	z	z		4	3269
6	RVYLHILWK		z	z	>	Z	Z		∢	3270
<b>o</b>	AMTESPTYK		zi	z	<b>&gt;</b> - :	Z:	Z		∢	3271
<b>o</b>	SWARAFPR		2 2	z	<b>&gt;-</b> :	Z:	z		∢	3272
<b>o</b> n (	SVVRRAFPK		Z 2	Z :	<b>&gt;</b> :	zz	zi		∢ ·	3273
<b>5</b> 1	SAIXSVVHH		2 2	z	<b>&gt;</b> ;	zz	2 >		⋖ •	32/4
ъ ;	LPVXAFSSA	3	2 2	Z :	z:	z	<b>≻</b> ∶	•	∢	32/3
0 9	FLLAGFTSAV	L2.IV10	Z 2	<b>&gt;</b> :	z:	z	z :	- :	∢	3276
2 9	YLFILWKAGI		Z 2	<b>&gt;</b> :	z	zz	zi	2 :	∢ -	3277
2 5	TLL LWRAGI		2 2	<b>&gt;</b> :	Z 2	Z 2	2 2	2 2	۷ ۰	3770
2 5	A GWENT A		: 2	- >	2 2	2 2	2 2	2 2	∢ «	2080
2 0	II VI OAGEEV	12.1 V10	: 2	- >	: 2	z	: Z	<u>}</u> -	( <	3281
9 0	ILLICITED V	L2.LV10	z	- >	: 2	: <b>z</b>	z	- <b>-</b>	( <	3282
20	FPFCLAFSYM		z	- z	: z	z	: >-	-	( ∢	3283
10	FPHCLAFSYI		z	z	z	Z	>-		< ⊲	3284
9	FPARVTGGVF		z	z	;, z	z	· <b>&gt;</b> -		< ∢	3285
10	TPFRVTGGVF		z	z	z	z	>		∶ ∢	3286
10	TPARVTGGVI		z	z	z	z	>		: ∢	3287
10	FPCALRFTSA		z	z	z	z	>		′ ∢	3288
0	GPFALRFTSA		z	z	z	z	>		4	3289
5	GPCALRFTSI		z	z	z	z	>		∢	3290
10	FPAAMPHLLV		Z	z	Z	z	>		∢	3291
			-							

Table XXII	5			HBV	/ ANALOGS					
4 4	Sequence	Fixed Nomen.	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	. 1° Anchor Fixer	Analog	SEQ ID NO:
10	HPFAMPHLLV		z	z	z	z	۶		4	3292
10	HPAAMPHLLI		z	z	z	z	<b>&gt;</b>		∶ ∢	3293
10	QMFTFSPTYK		z	z	>	z	z		∢	3294
9	QVFTFSPTYK		z	z	>-	z	z		•	3295
10	TMWKAGILYK		z	z	>-	z	z		∢	3296
10	TVWKAGILYK		Z	z	>-	z	z		∢	3297
10	VMGGVFLVDK		z	z	>-	z	Z		∢	3298
9 9	WGGVFLVDK		zi	z	<b>&gt;</b> :	Z:	Z:		∢	3299
10	SMLPETTVVR		2 ;	z	<b>&gt;</b> - :	Z :	Z:		∢	3300
0 9	SVLPETTVVR		zi	z	<b>&gt;</b> - :	z	z :		∢	3301
0 9	TMPETTVVRR		z	z	<b>&gt;</b> - :	z:	Z;		∢	3302
0 9	TVPETTWRR		zi	z	<b>&gt;</b> :	z	Z:		∢	3303
9	HTLWKAGILK		z	z	<b>&gt;</b> :	z	Z:		∢	3304
0 1	HTLWKAGILR		Z;	z	<b>&gt;</b> :	Z:	Z :		∢	3305
9	HMLWKAGILY		<b>≻</b>	z	<b>&gt;</b> :	z:	Z:		∢	3306
0 9	HVLWKAGILY		zi	z	<b>&gt;</b> :	z:	z:		∢	3307
0 9	GMDNSVVLSR		zz	Z	<b>&gt;-</b> :	z	z:		Α.	3308
0 :	GVDNSVVLSH		2 2	Z	<b>&gt;-</b> :	z:	z		∢	3309
Ç (	GTFNSVVLSR		zz	Z:	<b>&gt;</b> - :	z	z		¥	3310
2 ;	YMFDVVLGAK		2 2	zi	<b>-</b> >	zz	zz		⋖ ′	3311
2 \$	MANAMORPULA		zz	2 2	<b>&gt;</b> - >	2 2	z		⋖・	33.12
2 σ			: z	2 >	- 2	2 2	z z		∢ <	3314
, o	ירנאניי		z	- >	: Z	z	z		( ∢	3315
<b>.</b> 6	LIXUFLLV		z	- >-	: 2	z	z		·	3316
თ	PLLPIFFXL		z	>	z	z	z		: ∢	3317
თ	ALMPLYAXI		z	>	z	z	z		ď	3318
6	GLXQVFADA		z	<b>&gt;</b>	z	z	z		∢	3319
თ	HISXLTFGR		z	z	>-	z	z		¥	3320
თ	FVLGGXRHK		z	z	>-	z	z		ď	3321
10	FILLLXUFL		z	>	z	z	z		4	3322
9	ILLLXLIFIL		z	>	z	z	Z		∢	3323
2	re excifere v		z į	>	z	z	z		¥	3324
0	LLPIFFXLWV		z:	>-	z	z	z		∢	3325
0	OLLWFHISXL		Z :	>	z	z	z		¥	3326
0	LLGXAANWIL		Z	>	z	z	z		∢	3327
10	TSAIXSVVRR		Z	z	>	z	z		4	3328
0	GYRWMXLRRF		z	z	z	>-	z		∢	3329
10	GPXALRFTSA		z	z	z	z	>		∢	3330
10	FPHXLAFSYM		z	z	z	z	>		۷	3331
Ξ	HMLWKAGILYK		z	z	>-	z	z		∢	3332
Ξ	HVLWKAGILYK		z	z	>	z	z		⋖	3333

Table XXII	₽			HB	HBV ANALOGS					
A A	Sequence	Fixed Nomen.	A1 Motif	A2 Super	A3 Super	A24 Motif	B7 Super	1. Anchor	Analog	SEQ IC
]:	ogwatta mo		2	Motif	MOIII	2	Motif	Fixer		2334
= =	SWETELL VANA		: 2	2 2	- >	2 2	zz		∢ <	2224
	GMONSIANISBK		zz	Z 2	- >	2 2	zz		< <	3336
= =	GVDNSVVLSBK		z	zz	- >	: z	: z		( ∢	3337
Ξ	GTFNSVVLSRK		z	: 2	· <b>&gt;</b> -	z	z		< ∢	3338
80	MPLSYQHI		z	z	z	z	<b>&gt;</b>		< ∢	3339
80	LPIFFCLI		z	z	z	z	<b>&gt;</b>		: ∢	3340
ω	SPFLLAGI		z	z	z	z	>		< ≺	3341
œ	YPALMPLI		z	z	Z	z	>		∶ ∢	3342
ω	VPSALNPI		z	z	z	z	>		4	3343
თ	LPIFFCLWI		z	z	z	z	>		∢	3344
6	LPIHTAELI		z	z	z	z	>		∢	3345
10	VPFVQWFVGI		z	z	z	z	>		∢	3346
Ξ	NPLGFFPOHOI		Z	z	z	z	>		∢	3347
Ξ	LPIHTAELLAI	!	Z:	z	z	z	>		۷	3348
<b>o</b> (	FLPSYFPSA	L2.FY5.	zi	>	z	Z	Z	Rev3	∢	3349
<u></u>	YLHTWKAGV	, L2.IV10 ,	zz	<b>&gt;</b> :	Z :	zi	zi	-	٧	3350
Ξ,	SILPETYWAR		zi	Z	<b>&gt;</b> - :	2 :	Z		∢	3351
<b>o</b> o	YMDDVVLGV	MZ.AV9	z z	> :	zi	2 2	Z;	-	∢ •	3352
<b>o</b> n (	FPIPSSWAF		2 2	z:	z :	<b>z</b> ;	≻ ;		∢	3353
<b>o</b> n c	IPII SSWAF		2 2	zi	Z 2	2 2	<b>&gt;</b> >		∢ •	3354
n 0	FPVC: AFGV		z	2 2	2 2	2 2	- >		∢ <	3356
o	EPHCI AFAY		: z	2 2	2 2	2 2	- >		€ <	3357
ი	FPHCLAFSL		z	: z	z	z	· >-		( ∢	3358
6	IPIPMSWAF		z	z	z	z	>		∶ ∢	3359
6	FPHCLAFAL		z	z	z	z	<b>&gt;</b>		. ∢	3360
10	FLPSZFFPSV		z	>-	z	z	z	2	. ∢	3361
10	FLPSZFFPSV		z	>	z	z	z	<del>2</del>	∢	3362
თ	IPFPSSWAF		z:	z	z	z	<b>&gt;</b>		∢	3363
တ	IPIPSSWAI		z:	z	z	Z	<b>&gt;</b> :	-	∢	3364
o (	FPFCLAFSY		zi	z	Z	Z:	<b>&gt;</b> :		∢	3365
<b>o</b> (	FPHCLAFSI		z į	Z	Z:	z	<b>&gt;</b> :		∢	3366
<b>э</b> (	FPHCLAFSA		2 2	Z	Z :	z	<b>&gt;</b> :	•	∢	3367
° ,	FQPSDYFPSV		zi	> 1	Z:	Z:	Z:	Rev	∢	3368
<b>.</b>	YLLIMILI		z 2	<b>&gt;</b> :	z :	z	2 :		∢	3369
<b>o</b> n c	FLYIMILII		2 2	<b>&gt;</b> :	zi	zz	zz		∢ •	33/0
n c			2 2	≻ >	z 2	2 2	2 2		∢ ⋅	000
n -	FLLI RICTI		zz	>- Z	z >	2 2	2 2		∢ ∢	3372
: o	FU-SUFFFSVA FI PSOFFFPS		: z	2 2	<b>-</b> 2	2 2	? Z		∢ •	2273
n cc	H PSOFFP		z	2 2	2 2	2 2	2 2		∢ <	3375
,				2	-	:	:		٤	)

able XXII				HBV	HBV ANALOGS					
A A	Sequence	Fixed Nomen.	A 1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super	1° Anchor	Analog	SEO IC NO:
Ę	FI PSDFFPSI	L2 VI10	z	>	2	z	I N	Rev	4	3376
2 0	FLPSDYFPSV		z	- >	: 2	: 2	: z	£	( ⊲	3377
12	YSFLPSDFFPSV		z	- z	: 2	: z	z	2	( ∢	3378
10	YNMGLKFROL		z	z	z	z	z		< ∢	3379
6	NIMGLKYROL		z	: >-	z	>	z	2	< ∢	3380
10	FLPS(X)YFPSV		z	Z	z	z	z		: ∢	3381
10	FLPSD(X)FPSV		z	z	z	z	z		∶ ∢	3382
1	FLPSDLLPSVR		z	z	>-	Z	z		< <	3383
12	FLPSDFFPSVRD :		z	z	z	z	z		< <	3384
12	LSFLPSDFFPSV		z	z	z	z	z		4	3385
=	SFLPSDFFPSV		z	z	z	z	z		4	3386
œ	PSDFFPSV		z	z	z	z	z		∢	3387
6	FLMSYFPSV		z	>-	z	z	z	2	∢	3388
6	FLPSYFPSV	L2.FY5.	z	>	z	z	z	က	٧	3389
10	FLMSDYFPSV		z	>-	z	z	z	2	∢	3390
=	CILLICUFIL	-	z	>	z	z	z	2	∢	3391
10	FLPNDFFPSA	L2.5N4.	z	>	z	z	z	Rev	∢	3392
10	FLPDDFFPSA	L2.SD4.	z	>	z	z	z	Rev	∢	3393
10	FLPNDFFPSV		z	>	z	z	z	2	∢	3394
10	FLPSDFFPSA	L2.VA10	z	>	z	z	z	Rev	∢	3395
10	FLPDDFFPSV		z	>	z	z	z	2	∢	3396
0	FLPADFFPSV		z	>	z	z	z	2	∢	3397
9	FLPVDFFPSV		z	>	z	z	z	2	∢	3398
10	FLPADFFPSI	L2.SA4.	z	>	z	z	z	Rev	∢	3399
10	FLPVDFFPSI	L2.SV4.	z	>	z	z	z	Rev	∢	3400
10	FLPSDAFPSV		z	>	z	z	z	2	∢	3401
10	FLPSAFFPSV		z	>-	z	z	z	2	∢	3402
10	FLPSDFAPSV		z	>	z	z	z	2	∢	3403
10	FLPSDFFASV		z	>	z	z	z	2	∢	3404
10	FLPSDFFPAV		z	>	z	z	z	2	۷	3405
10	FLASDFFPSV		z	>-	z	z	z	2	∢	3406
10	FAPSDFFPSV	LA2.V10	z	>	z	z	z	Rev	∢	3407
10	ALPSDFFPSV		z.	>	z	z	z	2	∢	3408
10	YLPSDFFPSV		z	>	z	z	z	2	⋖	3409
10	FMPSDFFPSV	LM2.V1	z	>	z	z	z	-	∢	3410
10	FLKSDFFPSV		z	>-	z	z	z	2	⋖	3411
10	FLPSEFFPSV		z	>-	z	z	z	2	∢	3412
10	FLPSDFYPSV		z	>-	z	z	z	2	∢	3413
10	FLPSDFFKSV		z	>	z	z	z	2	∢	3414
9	FLPSDFFPKV		z	>	z	Z	z	2	∢	3415
	FLPSDFFPSV(CONH2)									3416
	VLEYLVSFGV(NH2)		-							3417

1 Analog SEQID Anchor NO: Fixer
B7 Super Motif
A24 Motif
Super Motif
Super Motif
A I Motif
Fixed Nomen.
Sequence
AA Sequ

HBV ANALOGS

Table XXII

Table XXIII: Immunogenicity of HBV-derived peptides

Supermotif         Peptide         Sequence           A2 supermotif         924.07         FLPSDFFBV           1069.06         LLVPFVQWFV           1147.13         FLLAQFTSAI           1090.77         YMDDVVLGV           777.03         FLLTRILTI           927.15         ALMPLYACI           1013.01         WLSLLVPFV           1132.01         LVPFVQWFV           1147.14         VLLDYQGMLPV           927.41         LLSSNLSWL           927.42         NLSWLSLDV           927.43         LLSSNLSWL           1147.14         VLLDYQGMLPV           927.41         LLSSNLSWL           927.42         NLSWLSLDV           927.43         KLHLYSHPII           1069.07         FLLAQFTSA           1168.02         GLSRYVARL           927.47         HLYSHPIIL           1039.03         MMWYWGPSL           1069.12         YLHTLWAGV           1142.07         GLLGWSPQA           1142.07         LLDYQGMLPV           1169.10         LLPIFFCLWV           1069.13         PLLPIFFCL           1069.13         PLLPIFFCL           1069.10         LLDYLQGGGGG <th>Ence SEQ ID NO:  FPSV 3493  QWFV 3494  FTSAI 3494  VLGV 3495  ULTI 3496  YACI 3497  VPFV 3498</th> <th>Protein HBV core 18</th> <th>XRN</th> <th>primary</th> <th>transgenic 6/6</th> <th>patients</th> <th>overall' +</th>	Ence SEQ ID NO:  FPSV 3493  QWFV 3494  FTSAI 3494  VLGV 3495  ULTI 3496  YACI 3497  VPFV 3498	Protein HBV core 18	XRN	primary	transgenic 6/6	patients	overall' +
924.07 1069.06 1147.13 1090.77 777.03 927.15 1013.01 1147.14 927.41 927.41 927.41 927.41 927.41 927.41 1069.07 1168.02 927.47 1168.02 1142.07 1142.07 110573 1013.14 1069.10		HBV core 18	,	10/10	9/9	BCCITC	+
1069.06 1147.13 1090.77 777.03 927.15 1013.01 1069.05 1132.01 1147.14 927.41 927.41 927.41 927.41 1069.07 1168.02 927.11 927.11 1069.12 1137.02 1142.07 1.0573 1069.10			1	21 22		75/57	
1147.13 1090.77 777.03 927.15 1013.01 1069.05 1132.01 1147.14 927.41 927.41 927.42 927.41 1069.07 1168.02 927.47 1039.03 1069.12 1142.07 1059.13 1069.13		HBV env 338	5	3/4	6/9		+
1090.77 777.03 927.15 1013.01 1069.05 1132.01 1147.14 927.41 927.41 927.42 927.41 927.47 1168.02 927.47 1168.02 1168.02 1168.01 1169.12 110573 11069.13		HBV pol 513	\$		0/3		nnk
777.03 927.15 1013.01 1069.05 1132.01 1147.14 927.41 927.45 1069.07 1168.02 927.11 927.11 927.11 927.11 1039.03 1069.12 1142.07 1.0573 1069.10		HBV pol 538	5		6/6		+
927.15 1013.01 1069.05 1132.01 1147.14 927.41 927.42 927.46 1069.07 1168.02 927.11 927.11 927.11 1039.03 1137.02 1142.07 1.0573 1069.10 1069.13		HBV env 183	4			14/23 <sup>a</sup>	+
1069.05 1132.01 1147.14 927.41 927.45 1069.07 1168.02 927.11 927.47 1039.03 1069.12 1142.07 1.0573 1069.10 1069.13		HBV pol 642	4	10/12	3/5	2/15 <sup>8</sup>	+
1069.05 1132.01 1147.14 927.41 927.45 1069.07 1168.02 927.11 927.11 927.47 1039.03 1069.12 1142.07 1.0573 1013.14 1069.13		HBV env 335	4	7/6	5/9	23/29 <sup>a</sup>	+
1132.01 1147.14 927.41 927.42 927.46 1069.07 1168.02 927.11 927.11 927.11 1039.03 1069.12 1142.07 1.0573 1069.10 1069.10	TSAI 3499	HBV pol 504	4	0/4	9/2		unk
1147.14 927.41 927.42 927.46 1069.07 1168.02 927.11 927.11 927.47 1039.03 1069.12 1142.07 1.0573 1069.10 1069.10	QWFV 3500	HBV env 339	4	0/3	0/4		nnk
927.41 927.42 927.46 1069.07 1168.02 927.11 927.47 . 1039.03 1069.12 1142.07 1.0573 1069.10 1069.13	GMLPV 3501	HBV env 259	4	4/4	9/9		+
927.42 927.46 1069.07 1168.02 927.11 927.47 . 1039.03 1069.12 1137.02 1142.07 1.0573 1013.14 1069.13	LSWL 3502	HBV pol 992	3	0/4	0/3		nnk
927.46 1069.07 1168.02 927.11 927.47 . 1039.03 1069.12 1137.02 1142.07 1.0573 1013.14 1069.10 1069.13	SLDV 3503	HBV pol 411	3		2/8		+
1069.07 1168.02 927.11 927.47 . 1039.03 1069.12 1137.02 1142.07 1.0573 1013.14 1069.10 1069.13	rshpi 3504	HBV pol 489	٣	0/4	4/6		+
927.11 927.47 . 1039.03 1069.12 1137.02 1142.07 1.0573 1013.14 1069.10 1090.06	FTSA 3505	HBV pol 503	3	1/2	0/3		+
927.11 927.47 . 1039.03 1069.12 1137.02 1142.07 1.0573 1013.14 1069.13	VARL 3506	HBV pol 455	3			9/13 <sup>a</sup>	+
	GIHL 3507	HBV pol 562	2	15/22	12/13	81/6	+
	HPIIL 3508	HBV pol 1076	2		10/14		+
	WGPSL 3509	HBV env 360	2	3/4	0/4		+
	VKAGV 3510	HBV pol 147	2	2/4			+
	SMLPV 3511	HBV env 260	2	7/1	0/4		+
	/SPQA 3512	HBV env 62	2	3/4	9/9		+
	SFVYV 3513	HBV pol 773	,			3/7	+
	JFFLL 3514	HBV env 177		0/4	5/12		+
	CLWV 3515	HBV env 378	_	3/3	0/4	2/5°	+
	FFCL 3516	HBV env 377	-	0/4	7/12		+
	AGFFL 3517	HBV env 175	_	1/5	0/4		+
1090.12 YLVSFGVWI	GVWI 13518	HBV nuc 118	-	6/6			+
1.0518 GLSPTVWLSV	/WLSV 3519	HBV env 338	_			3/9°	+
1090.14 YMDDVVLGA	VVLGA 3520	HBV pol 538	1	7/2	2/5	2/7	+
A3 supermotif 1147.16 HTLWKAGILYK	AGILYK 3521	HBV POL 149	\$	9/0	3/3	1/22	+
1083.01 STLPETTVVRR	TVVRR 3522	HBV core 141	4	3/5	9/9	8/32	+
1150.51 GSTHVSWPK	/SWPK 3523	HBV pol 398	4		3/6		+
1.0219 FVLGGCRHK	JCRHK 3524	HBV adr "X" 1550	e	0/4			nuk
1069.16 NVSIPWTHK	WTHK 3525	HBV pol 47	ъ	8/0	0/3	1/21	+

+	+	+	+	+	+	+	+	nnk	+	nnk	nnk	+
. 1/22	3/21	2722	5/28	222	0/12	2/16	1/12	0/12		0/12		2/12
9/9	0/3	•	0/3	. 6/3								=
0/4	3/6	1/4	3/8		1/3		0/4	9/2	1/4		0/4	
33	33	3	2	2	5	4	4	4	4	4	3	2
HBV pol 388	HBV pol 665	HBV pol 531	HBV pol 150	HBV adr POL 629	HBV POL 530	HBV core 19-27	HBV ENV 313	HBV POL 429	HBV X 58	HBV POL 640	HBV POL 541	HBV POL 354
3526	3527	3528	3529	3530	3531	3532	3533	3534	3535	3536	3537	3538
LVVDFSQFSR	QAFTFSPTYK	SAICSVVRR	TLWKAGILYK	KVGNFTGLY	FPHCLAFSYM	LPSDFFPSV	IPIPSSWAF	HPAAMPHLL	LPVCAFSSA	YPALMPLYA	FPHCLAFSYM	TPARVTGGVF
1069.20	1090.10	1090.11	1069.15	1142.05	1147.05	988.05	1145.04	1147.02	1147.06	1147.08	1145.08	1147.04
			A3 supermotif		B7 supermotif							B7 supermotif

Immunogenicity evaluation derived from primary cultures, acute patients (a-Bertoni et al, J Clin Invest 100:503, b- Rehermann et al., J. Clin. Invest 97:1655, c- Nayersina et al., J Immunol 150:4659) or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. Unk=unknown

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

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			•	Radiolal	Radiolabeled peptide		
Species	Antigen	Allele	Cell line	Source	Sequence	SEQ ID NO:	
Human	ΑI	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	3539	
	A2	A*0201	Л	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	3540	
	<b>A</b> 3		GM3107	non-natural (A3CON1)	KVFPYALINK	3541	
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	3541	
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF	3542	
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	3541	
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	3541	
	A28/68	A*6801	CIR	HBVc 141-151 T7->Y	STLPETYVVRR	3543	
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	3544	
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLVYLL	3545	
	B8	B*0801	Steinlin	HIVgp 586-593 Y1->F, Q5->Y	FLKDYQLL	3546	
	B27	B*2705	TC2	R 60s	FRYNGLIHR	3547	
	B35.	B*3501	CIR, BVR	non-natural (B35CON2)	FPFKYAAAF	3548	
	B35	B*3502	TISI	non-natural (B35CON2)	<b>FPFKYAAAF</b>	3548	
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF	3548	
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	3549	
	B51		KAS116	non-natural (B35CON2)	<b>FPFKYAAAF</b>	3550	•
	B53	B*5301	AMAI	non-natural (B35CON2)	<b>FPFKYAAAF</b>	3550	
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF	3550	
	Cw4	Cw*0401	CIR	non-natural (C4CON1)	QYDDAVYKL	3551	
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	3552	
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	3552	
Mouse	Ω		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	3553	
	K <sup>p</sup>		EL4	VSV NP 52-59	RGYVFQGL	3554	
	Dq	•	P815	HIV-IIIB ENV G4->Y	RGPYRAFVTI	3555	
	Κ <sub>q</sub>		P815	non-natural (KdCON1)	KFNPMKTYI	3556	
	F <sub>J</sub>		P815	HBVs 28-39	PQSLDSYWTSL	3557	

SEO ID NO: 3568 3569 3566 3566 3567 3570 3572 3559 3571 АНААНААНААНАА **АНААНААНААНАА** АНААНААНААНАА АНААНААНААНАА АНААНААНААНАА YNTDGSTDYGILQINSR YLEDARRKKAIYEKKK YLEDARRKKAIYEKKK /VHFFKNIVTPRTPPY EALIHQLKINPYVLS YARFQSQTTLKQKT YPKYVKQNTLKLAT YAAFAAAKTAAAFA YARFQSQTTLKQKT YARFOSOTTLKOKT YARFQRQTTLKAAA YARFQSQTTLKQKT PKYVKQNTLKLAT QYIKANSKFIGITE **OYIKANAKFIGITE** QYIKANAKFIGITE QYIKANSKFIGITE QYIKANSKFIGITE QYIKANSKFIGITE **QYIKANSKFIGITE** NGQIGNDPNRDIL YKTIAFDEEARR Sequence Radiolabeled peptide ambda repressor 12-26 Lambda repressor 12-26 unknown eluted peptide Tet. tox. 830-843 S->A non-natural (ROIV) non-natural (717.01) non-natural (ROIV) non-natural (ROIV) non-natural (717.10) non-natural (717.01) non-natural (717.01) non-natural (ROIV) non-natural (760.16) 10n-natural (717.01) non-natural (ROIV Tet. tox. 830-843 Tet. tox. 830-843 Tet. tox. 830-843 Tet. tox. 830-843 Tet. tox. 830-843 MT 65kD Y3-13 Tet. tox. 830-843 Tet. tox. 830-843 HA Y307-319 MBP 88-102Y HA 307-319 HEL 46-61 Source GM3107 or L416.3 .S102.9 L257.6 **DB27.4** 1242.5 3IN 40 Sweig Herluf H0301 L255.1 CH-12 Pitout Preiss A20 .466.1 YAR KT3 MAT A20 91.7 MAT OLL LUY H QA1\*0301/DQB1\*03( DRB1 \*0405 DRB1 \*0802 DRB1\*0803 **JRB1\*1302** DRB5\*0101 DRB5\*0201 DRB3\*0101 DRB4\*0101 ORB1\*1601 DRB1 \*0401 DRB1 \*0404 DRB1\*0701 DRB1\*1101 JRB1\*1501 DRB1 \*0301 DRB1\*0402 DRB1\*0901 JRB1\*1201 B. Class II binding assays **DR4w15** DR4w14 DR51: DR4w4 DR4w10 DR52 DR13 D03.1 DR12 DRS1 DR53 DR9 DR2 DR3 DR7 DR8 DR8 DRII Mouse Species Human

Table XXV. Monoclonal antibodies used in MHC purifi

Monoclonal antibody	Specificity
W6/32	HLA-class I
B123.2	HLA-B and C
IVD12	HLA-DQ
LB3.1	HLA-DR
M1/42	H-2 class I
28-14-8S	$H-2 D^b$ and $L^d$
34-5-8S	H-2 D <sup>d</sup>
B8-24-3	H-2 K <sup>b</sup>
SF1-1.1.1	H-2 K <sup>d</sup>
Y-3	H-2 K <sup>b</sup>
10.3.6	H-2 IA <sup>k</sup>
14.4.4	$H-2 IE^d, IE^K$
MKD6	H-2 IA <sup>d</sup>
Y3JP	H-2 IA <sup>b</sup> , IA <sup>s</sup> , IA <sup>u</sup>

Table XXVI: in vitro binding of conserved HBV-derived peptides to HLA-A2-supertype alleles.

								A2-supertype	A2-supertype binding capacity (IC50 nM)	ity (IC50 nM)		Alleles
Peptide	¥	Molecule	1st Pos	Sequence	SEQ ID NO:	Consv.	A*0201	A*0202	A*0203	A*0206	A*6802	bound 5
924.07	9	Core	81	FLPSDFFPSV	3492	95	2.5	2.1	6.0	3.0	36	~
1069.06	9	EN	349	LLVPFVQWFV	3493	95	7.5	=	5.9	13	286	~
1147.13	0	POL	524	FLLAQFTSAI	3494	95	24	134	4.1	34	455	S
1013.0102	6	EN	346	WLSLLVPFV	3498	100	4.6	113	1.4	01	1290	4
777.03	0	ENA	183	FLLTRILTI	3496	80	8.6	81	1.3	61	۳,	4
927.15	6	POL	653	ALMPLYACI	3497	95	01	126	3.0	160	851	4
1069.05	6	POL	525	LLAQFTSAI	3499	95	20	16	3.0	1538	51	4
1132.01	6	ENA	350	LVPFVQWFV	3500	95	611	287	2083	463	14	4
1147.14	=	EN	259	VLLDYQGMLPV	3501	8	9.8	20	2.0	13	2353	4
1090.77	6	POL	538 (a)	YMDDVVLGV	3495	8	5.1	8	6.7	11	1905	4
1069.01	6	POL	524	FLLAQFTSA	3505	95	0.9	1654	9.1	39	870	m
927.46	6	POL	200	KLHLYSHPI	3504	95	72	126	3.7	. 627	26667	٣
. 927.42	6	PQ.	422	NLSWLSLDV	3503	06	11	843	91	2313	404	m
1168.02	6	δĹ	455	GLSRYVARL	3506	06	79	391	18	12333		М
927.41	6	POL	418	LLSSNLSWL	3502	06	455	55	2.6	1370	4000	٣
1039.031	6	EN	360	MMWYWGPSL	3509	88	5.6	5375	833	112	3636	2
927.11	6	POL	573	FLLSLGIHL	3507	95	1.7	4300	0001	34	11429	7
1142.07	6	EN.	52	GLLGWSPQA	3512	82	13	14333	286	1429	•	7
927.47	•	POL	202	HLYSHPIIL	3508	80	23	14333	=	2176	755	7
1137.02	2	EN	. 27I	LLDYQGMLPV	3511	8	51	•	200	552		7
1069.09	6	EN	270	VLLDYQGML	3573	95	114		476	4111		7
1069.14	2	NUC	168	ILSTLPETTV	3574	001	238	206	130	1194	5970	2
106901	2	POL	147	YLHTLWKAGI	3575	<u>8</u>	313	8600	18	4000	1250	7
1142.01	6	NUC	129	LLWFHISCL	3576	8	385	21500	238	1194	4082	2
1090.12	6	NUC	147	YLVSFGVWI	3518	8	13					_
1.0518	9	EN	329	GLSPTVWLSV	3519	75	81					-
1013.1402	6	EN	111	VLQAGFFLL	3514	95	33	2389	3704	1947	6349	-
1069.13	6	EN	388	PLLPIFFCL	3516	<u>8</u>	11	•	5556	3364	8511	_
1069.10	9	EN	389	LLPIFFCLWV	3515	100	156	5375	199	2000	•	-
1090.06	9	EN	175	LLVLQAGFFL	3517	96	191	1162	2222	2467	3636	-
1.0895	01	ENA	248	FILLICLIFL	3577	8	179					-
927.24	6	POL	770	WILRGTSFV	3578	80	185					-
1090.14	6	POL	538	YMDDVVLGA	3520	8	200		4167		•	_
3.0205	2	ENA	121	FLGPLLVLQA	3579	75	263					<b>-</b>
1069.08	2	ENA	260	ILLLCLIFIL	3580	8	263	•		2846	26667	-
1.0573	2	POL	773	ILRGTSFVYV	3581	80	313					-

Frequency of entire sequence amongst isolates scanned.
 Number of supertpe alleles bound. Peptides binding 3 or more alleles are considered degenerate.
 A dash (-) indicates IC50

Table XXVII: in vitro binding of conserved HBV-derived peptides to HLA-A3-supertype alleles.

Peptide	¥	Molecule	1st Pos	Sequence	SEQ ID NO:	Consv.	A•03	N•11	A*3101	A*3301	A*6801	punoq
26.0535	=	X NUC FUS	599	GVWIRTPPAYR	3582	25	58	35	3.0	40	12	~
1147.16	=	log.	149	HTLWKAGILYK	3583	001	70	14	486	403	45	S
26.0539	=	POL	376	RLVVDFSQFSR	3584	95	39	5.0	7.0	24	0.	S
26.0149	6	×	69	CALRFTSAR	3585	85	3235	197	12	3.6	=	4
1.0993	٥	×	130	KVFVLGGCR	3586	75	262	73	30	408	2992	4
26.0153	6	×	64	SSAGPCALR	3587	8	1375	43	55	181	=	4
1083.01	=	Core	141	STLPETTVVRR	3588	98	733	4.0	081	181	56	4
20.0130	6	pol	655	AFTFSPTYK	3589	95	42	120	3103	13182	596	٣
26.0008	90	POL	959	FTFSPTYK	3590	95	193	136	1286	1000	7.3	٣
1.0219	6	×	1550	FVLGGCRHK	3591	8	691	316	1500	744	103	٣
1069.20	<u>o</u>	POL	388	LVVDFSQFSR	3592	100	6875	11	692	126	91	æ
91.6901	6	POL	47	NVSIPWTHK	3593	001	134	105	۳,	2900	250	٣
1090.10	2	POL	999	QAFTFSPTYK	3594	\$6	244	=	18000	5088	6.7	
1090.11	6	POL	531	SAICSVVRR	3595	95	1897	53	1200	446	71	٣
20.0131	6	<u>8</u>	524	SVVRRAFPH	3596	95	100	2	621		200	e
26.0545	=	X NUC FUS	318	TLPETTVVRRR	3597	98	22000	375	2951	408	<u>:</u>	3
26.0023	8	X NUC FUS	596	VSFGVWIR	3598	06	2750	207	240	1074	222	3
1142.05	6	POL	55	KVGNFTGLY	3599	56	52	353		•		2
1142.06	6	<b>7</b> 0L	623	PVNRPIDWK	3600	88	355	43		•	8889	7
1.0975	6	POL	901	RLKLIMPAR	3601	75	116		5.8	592		7
1.0562	2	POL	576	SLGIHLNPNK	3602	75	55	μ				7
1069.21	9	NUC	170	STLPETTVVR	3603	98	15714	<u>8</u>	2250	1208	320	7
1069.22	2	NUC	17	TLPETTVVRR	3604	95	15714	761	•	2417	182	7
1069.15	2	POL	120	TLWKAGILYK	3605	100	2.1	11	3529	29000	615	7
1.0215	6	×	105	TTDLEAYFK	3606	75	18333	6.5	٠	24167	471	7
1069.17	<u>°</u>	POL	369	VTGGVFLVDK	3607	<u>0</u>	282	\$9		٠	3636	7
1069.19	6	POL	389	VVDFSQFSR	3608	<u>00</u>	7333	8	13846	1706	242	7
26.0026	<b>∞</b>	POL	168	ASFCGSPY	3609	100	239	92	•		20000	7
26.0549	=	ENA	389	LLPIFFCLWVY	3610	100	478	10000	5609	644	83	7
26.0550	Ξ	POL	828	RAFPHCLAFSY	3611	98	92	15	<b>199</b>	26364	7997	7
1090.04	9	POL	746	GTDNSVVLSR	3612	8	11000	.143	0009	15263	10000	-
1069.04	2	POL	149	HTLWKAGILY	3613	8	250	7500		8529	1999	-
1.0205	6	POL	171	ILRGTSFVY	3614	08	250	•	•	•	•	-
1090.08	6	NUC	148	LVSFGVWIR	3615	06	3929	200				-
1039.01	2	EN	360	MMWYWGPSLY	3616	82	220	7500	•		79997	-
1.0584	2	×	104	STTDLEAYFK	3617	75	1991	2.2				-
1147.17	=	<u>100</u>	735	GTDNSVVLSRK	3618	9	786	=	•	•		-
1147.18	=	lod	357	RVTGGVFLVDK	3619	001	878	207		•	•	-
1099.03	6	70 <u>r</u>	120	TLWKAGILY	3620	100	85	7500			•	-
1090.15	9	POL .	549	YMDDVVLGAK	3621	06	333	1395	•		•	-
7000 70	•											

Frequency of entire sequence amongst isolates scanned.
 Number of superipe alleles bound. Peptides binding 3 or more alleles are considered degenerate.
 A dash (-) indicates IC50

Table XXVIII: in vitro binding of conserved HBV-derived peptides to HLA-B7 supertype alleles.

							Œ.	7-supertype l	binding capac	B7-supertype binding capacity (IC50 nM)	0	Alleles
Peptide	¥	Molecule	1st Pos	Sequence	SEQ ID NO: Consv.	Consv.	B•0702	B*3501	B*5101	B*5301	B*5401	bound 2
1147.05	2	POL	541	FPHCLAFSYM	3623	95	<b>S6</b>	33	19	118	208	~
1145.04	6	ENA	324	IPIPSSWAF	3624	8	42	5.6	2.3	. 21	2941	4
1147.02	6	POL	440	HPAAMPHILL	3625	001	98	267	200	981	833	4
1147.06	6	×	28	LPVCAFSSA	3626	95	115	101	200	10333	0.53	4
1147.08	6	POL	159	YPALMPLYA	3627	95	306	120	162	664	0.63	4
988.05	6	CORE	61	LPSDFFPSV	3628	95	1774	343	9.0	120	8.	4
1145.08	6	POL	541	FPHCLAFSY	3629	95	Μ,	14	. 8	11	503	ю
19.0014	90	POL	640	YPALMPLY	3630	180	13750	28	13	207	1786	٣
26.0570	=	lod	640	YPALMPLYACI	3631	95	1375	•	117	291	143	m
1147.04	01	POL	365	TPARVTGGVF	3632	06	11	72		939	19991	2
15.0034	6	ENA	330	LPIFFCLWV	3633	901			57	2325	23	7
20.0140	6	POL	723	LPIHTAELL	3634	82	1375	114	1058	30	20000	7
9000'61	<b>∞</b>	ENA	340	VPFVQWFV	3635	95	2200		0.29	•	16	7
19.0007	90	ENA	379	LPIFFCLW	3636	<u>8</u>		•	153	99	2857	7
19.0010	00	POL	_	MPLSYQHF	3637	001	•	742	458	251	226	7
19.0011	∞	POL	429	HPAAMPHL	3638	90	88	18000	81	2514	625	2
19.0012	∞	POL	511	SPFLLAQF	3639	95	01	8000	306	10333	1075	7
26.0566	=	ю Г	511	SPFLLAQFTSA	3640	95	29			•	0.83	7
1147.01	0	POL	789	DPSRGRLGL	3641	8	458	•	•	•		
16.0182	2	×	19	GPCALRFTSA	3642	8	19		•		2857	-
20.0273	2	POL	440	HPAAMPHLLV	3643	82	344	3600	705	664	588	-
15.0030	6	EN	161	IPQSLDSWW	3644	8		•	27500	62		_
15.0210	2	POL	123	LPLDKGIKPY	3645	<u>8</u>		248	27500		•	_
16.0006	•	ENA	22	FPDHQLDPA	3646	8		8000			13	_
16.0177	2	EN	324	IPIPSSWAFA	3647	8	4231	3000		6643	22	-
16.0180	2	POL	644	APFTQCGYPA	3648	8	1897				7.1	_
16.0181	2	POL	723	LPIHTAELLA	3649	82	3056	6545		5813	39	_
19.0003	∞	ENA	173	GPLLVLQA	3650	95	18333		200		1538	_
19.0005	∞	EN	313	IPIPSSWA	3651	001	13750	18000	2895	•	167	_
19.0009	<b>∞</b>	NUC	133	RPPNAPIL	3652	<u>00</u>	724	•	961			-
19.0015	<b>∞</b>	POL	629	SPTYKAFL	3653	95	4	•	2895	•	•	-
9100'61	••	POL	692	VPSALNPA	3654	8	2000	•	786		2	_
26.0554	=	2	633	, APFTQCGYPAL	3655	95	24	7200	13750	•	1075	-
26.0559	=	2	712	LPIHTAELLAA	3656	82	119	2667	•	27.5	3.6	_
26.0561	=	8	174	NPADDPSRGRL	3657	8	428	•	•	•		_
26.0564	=	Core	133	RPPNAPILSTL	3658	<u>8</u>	42	•	3056	•		_
26.0567	=	Core	49	SPHHTALRQAI	.3659	8	9.5	•	13750	18600	•	_
26.0568	=	pol	354	TPARVTGGVFL	3660	96	88	•	•	18600	20000	_

Frequency of entire sequence amongst isolates scanned.
 Number of superpe alleles bound. Peptides binding 3 or more alleles are considered degenerate.
 A dash (-) indicates IC50

Table XXIX: HBV derived A1- and A24-motif containing peptides

a. A1-motif peptides

D .: 1	) / - l l -	Panisia		SEO ID NO.	Company	HLA-A*0101
Peptide	Molecule	Position	Sequence	SEQ ID NO:	Conserv.	binding (IC50 nM)
1069.01	Core	59	LLDTASALY	3661	75	2.1
1.0519	Core	419	DLLDTASALY	3662	75	2.3
1069.02	pol	427	SLDVSAAFY	3663	95	4.8
2.0239		1000	LSLDVSAAFY	3664	95	6.0
2.0126		1521	<b>MSTTDLEAY</b>	3665	75	29
1039.06	ENV	359	WMMWYWGPSLY	3666 ·	. 85	78
1090.14	pol	538	YMDDVVLGA	3667	90	96
1090.09	pol	808	PTTGRTSLY	3668	85	119
1069.03	pol	124	PLDKGIKPYY	3669	100	147
1069.08	env	249	ILLLCLIFLL	3670	100	192
1069.04	pol	149	HTLWKAGILY	3671	100	381
1039.01	•	360	MMWYWGPSLY	3672	85	309
1.0774	Core	416	WLWGMDIDPY	3673	75	309
20.0254	pol	631	FAAPFTQCGY	3674	95	368
1.0166	pol	629	KVGNFTGLY	3675	95	368

A dash indicates IC50 nM

b. A24 -motif peptides

Peptide	Molecule	Position	Sequence	SEQ ID NO:	Conserv.	HLA-A*2402 binding (IC50 nM)
20.0271	POL	392	SWPKFAVPNL	3676	95	2.1
1069.23	POL	745	KYTSFPWLL	3677	85	2.3
2.0181	POL	492	LYSHPIILGF	3678	80	11
20.0269	ENV	236	RWMCLRRFII	3679	95	11
20.0136	ENV	334	SWLSLLVPF	3680	100	31
20.0137	ENV	197	SWWTSLNFL	3681	95	32
20.0135	ENV	236	RWMCLRRFI	3682	95	169
20.0139	POL	167	SFCGSPYSW	3683	100	169
2.0173	POL	4	SYQHFRKLLL	3684	75	182
2.0060		1224	GYPALMPLY	3685	95	245
13.0129	NUC	117	<b>EYLVSFGVWI</b>	3686	90	353
1090.02	core	131	AYRPPNAPI	3687	90	387
13.0073	NUC	102	WFHISCLTF	3688	80	400
20.0138	POL	51	PWTHKVGNF	3689	100	414

A dash indicates IC50 nM

overall Table XXXa: Immunogenicity of HBV-derived A2-supermotif cross-reactive peptides patients 23/29<sup>a</sup> 9/13<sup>a</sup> 14/23ª 2/15<sup>a</sup> Immunogenicity transgenic 6/9 0/3 6/6 2/9 0/2 9/4 9/9 0/3 2/8 4/6 63 primary 10/12 10/10 0/4 12 0/4 4/4 0/4 6/3 XRN HBV env 338 HBV env 335 HBV env 339 HBV env 259 HBV pol 411 HBV pol 489 HBV pol 503 HBV pol 455 HBV pol.538 HBV env 183 HBV pol 642 HBV pol 504 HBV pol 992 HBV core 18 HBV pol 513 Protein SEQ ID NO: 3696 3697 3698 3699 3700 3702 3703 3704 3692 3693 3694 3695 3701 3691 VLLDYQGMLPV LVPFVQWFV YMDDVVLGV LVPFVQWFV NLSWLSLDV GLSRYVARL FLPSDFFPSV FLLAQFTSAI WLSLLVPFV LLSSNLSWL FLLAQFTSA ALMPLYACI LLAQFTSAI KLHLYSHPI Sequence FLLTRILTI 1168.02 1147.14 Peptide 1069.06 1069.05 1147.13 1090.77 1013.01 1132.01 927.46 . 1069.07 927.15 927.42 924.07 777.03 927.41

Invest 97:1655, c- Nayersina et al., J Immunol 150:4659) or transgenic mice. A positive assessment (+) is assigned when responders have been Immunogenicity evaluation derived from primary cultures, acute patients (a-Bertoni et al, J Clin Invest 100:503, b- Rehermann et al., J. Clin. noted in one of these systems.

I	Table XXXb: In	nmunogenicit	XXXb: Immunogenicity of non-crossreactive HBV A2-supermotif peptides	active H	<b>BV A2-s</b>	upermotif	peptides	
						Immunogenicity	genicity	
Peptide	Sequence	SEQ ID NO:	Protein	XRN	primary	transgenic	patients	overall <sup>1</sup>
927.11	FLLSLGIHL	3705	HBV pol 562	2	15/22	12/13	9/15 <sup>a</sup>	+
927.47	HLYSHPIIL	3706	HBV pol 1076	2		10/14		+
1039.03	MMWYWGPSL	3707	HBV env 360	2	3/4	. 0/4		+
1069.12	YLHTLWKAGV	3708	HBV pol 147	<b>5</b> .	2/4			+
1137.02	LLDYQGMLPV	3709	HBV env 260	2	1/2	9/4		+
1142.07	GLLGWSPQA	3710	HBV env 62	2	3/4	9/9		+
1.0573	ILRGTSFVYV	3711	HBV pol 773	_			3/7 <sup>b</sup>	+
1013.14	VLQAGFFLL	3712	HBV env 177		0/4	5/12		+
1069.10	LLPIFFCLWV	3713	HBV env 378	-	3/3	0/4	2/5°	+
1069.13	PLLPIFFCL	3714	HBV env 377	-	9/4	7/12		+
1090.06	LLVLQAGFFL	3715	HBV env 175	-	1/5	0/4		+
1090.12	YLVSFGVWI	3716	HBV nuc 118	_	6/6			+
1.0518	GLSPTVWLSV	3717	HBV env 338	-			3/9 <sup>c</sup>	+
1090.14	YMDDVVLGA	3718	HBV pol 538	1	7/7	2/5	2/7 <sup>b</sup>	+

Immunogenicity evaluation derived from primary cultures, acute patients (a-Bertoni et al, J Clin Invest 100:503, b- Rehermann et al., J. Clin. Invest 97:1655, c- Nayersina et al., J Immunol 150:4659) or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems.

Table XXXc: Cross-recognition of HBV pol 538 and a Lamivudine induced pol 538 variant by CTL induced with a pol 538 analog<sup>a</sup>.

Day 6 CTL response (ALU)	HBV pol 538 mutant (YVDDVVLGA)	C 7 3	74.C	27.9
Day 6	HBV pol 538 (YMDDVVLGA)	0 7 7	8.77	35.3
	Stimulating peptide		HBV pol 538	HBV pol 538 mutant

a. CTLs were induced using the 1090.77 analog of HBV pol 538 (peptide 1090.14). 1090.77 was encoded in the DNA minigene pEP2.AOS.

b. Values shown represent the geometric mean of ALU from 2 independent cultures. Peptides loaded onto target cells were 1090.14 (HBV pol 538) or 1353.02 (a Lamivudine induced mutant of pol 538).

Table XXXIa: Immunogenicity of HBV-derived A3-supermotif cross-reactive peptides

						Immunogenicity	genicity	
Peptide	Sequence	SEQ ID NO:	Protein	XRN	primary	transgenic	patients	overall <sup>1</sup>
1147.16	HTLWKAGILYK	3719	HBV POL 149	5	9/0	3/3	1/22	+
1083.01	STLPETTVVRR	3720	HBV core 141	4	3/5	9/9	8/32	+
1150.51	GSTHVSWPK	3721	HBV pol 398	4		3/6		+
1.0219	FVLGGCRHK	3722	HBV adr "X" 1550	33	0/4			•
1069.16	NVSIPWTHK	3723	HBV pol 47	т	8/0	0/3	1/21	+
1069.20	LVVDFSQFSR	3724	HBV pol 388	ო	0/4	9/9	1/22	+
1090.10	QAFTFSPTYK	3725	HBV pol 665	က	3/6	0/3	3/21	+
1090.11	SAICSVVRR	3726	HBV pol 531	3	1/4		2/22	+

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined. Table XXXIb: Immunogenicity of non-crossreactive HBV A3-supermotif peptides

meny	patients overall1	5/28 +	2/22 +
minimogenicity	transgenic patients	6/3	0/3
	XRN primary	3/8	:
•	XRN	2	2
	Protein	HBV pol 150	HBV adr POL 629
	SEQ ID NO:	3727	3728
	Sequence	TLWKAGILYK	KVGNFTGLY
	Peptide	1069.15	1142.05

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined. Table XXXIIa: Immunogenicity of HBV B7-supermotif cross-reactive peptides

				•		Immunogenicity	genicity	
Peptide	Sequence	SEQ ID NO:	Protein	XRN	primary	XRN primary transgenic patients overall	patients	overall
1147.05	FPHCLAFSYM	3729	HBV POL 530	5	1/3		0/12	+
988.05	LPSDFFPSV	3730	HBV core 19-27	4			2/16	+
1145.04	IPIPSSWAF	3731	HBV ENV 313	4	0/4		1/12	+
1147.02	HPAAMPHLL	3732	HBV POL 429	4	0/5		0/12	1
1147.06	LPVCAFSSA	3733	HBV X 58	4	1/4			+
1147.08	YPALMPLYA	3734	HBV POL 640	4			0/12	•
1145.08	FPHCLAFSY	3735	HBV POL 541	m	0/4			1

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined. Table XXXIIb: Immunogenicity of non-crossreactive HBV B7-supermotif peptides

	rall		
	overall		
genicity	patients	2/12	
Immunogenicity	transgenic		
	primary		
•	XRN	2	
	Protein	HBV POL 354	
	SEQ ID NO:	3736	
	Sequence	TPARVTGGVF	
	Peptide	1147.04	

1. Immunogenicity evaluation derived from primary cultures, Bertoni et al, J Clin Invest 100:503 or transgenic mice. A positive assessment (+) is assigned when responders have been noted in one of these systems. A negative assessment (-) indicates that no responders when examined.

## Table XXXIII. Candidate HBV-derived HTL epitopes

Selection				Conse	rvancy		•
criteria	Peptide	Mol	1st Pos	Core	Total	Sequence	SEQ ID NO
DR-supermotif	F107.01	ENV	249	100	95	ILLLCLIFLLVLLDY	3737
	F107.02	ENV	252	95	95	LCLIFLLVLLDYQGM	3738
	1280.17	ENV	258	90	90	LVLLDYQGMLPVCPL	3739
	1186.22	ENV	332	100	100	RFSWLSLLVPFVQWF	3740
	1186.15	ENV	339	95	95	LVPFVQWFVGLSPTV	3741
	1186.06	ENV	342	95	95	<b>FVQWFVGLSPTVWLS</b>	3742
	1186.03	NUC	19	85	85	ASKLCLGWLWGMDID	3743
	1186.12	NUC	24	85	85	LGWLWGMDIDPYKEF	r 3744
	857.02	NUC	50		90	PHHTALRQAILCWGELMTLA	3745
	1186.23	NUC	98	85	85	RQLLWFHISCLTFGR	3746
	27.0279	NUC	117		90	<b>EYLVSFGVWIRTPPA</b>	3747
	27.0280	NUC	123	95	95	GVWIRTPPAYRPPNA	3748
	1186.20	NUC	129	100	95	PPAYRPPNAPILSTL	3749
	1186.16	NUC	136	100	95	NAPILSTLPETTVVR	3750
	1186.01	POL	38	95	95	<b>AEDLNLGNLNVSIPW</b>	3751
	1186.17	POL	45	100	95	NLNVSIPWTHKVGNF	3752
	27.0281	POL	145	100	100	RHYLHTLWKAGILYK	3753
	1280.13	POL	406	95	95	KFAVPNLQSLTNLLS	3754
	27.0283	POL	409		85	VPNLQSLTNLLSSNL	3755
	F107.03	POL	412	90	90	LQSLTNLLSSNLSWL	3756
	1186.28	POL	416	90	90	TNLLSSNLSWLSLDV	3757
	1186.27	POL	420	100	85	SSNLSWLSLDVSAAF	3758
	F107.04	POL	523	95	95	PFLLAQFTSAICSVV	3759
	1186.10	POL	526	95	95	LAQFTSAICSVVRRA	3760
	1186.04	POL	534	95	95	CSVVRRAFPHCLAFS	3761
	F107.05	POL	538	95	95	RRAFPHCLAFSYMDD	3762
	1186.02	POL	546	90	90	AFSYMDDVVLGAKSV	3763
	1186.05	POL	629	85	85	DWKVCQRIVGLLGFA	3764
	1280.21	POL	637	95	95	VGLLGFAAPFTQCGY	3765
	27.0278	POL	643	75	95	AAPFTQCGYPALMPL	3766
	1186.21	POL	648	95	95	QCGYPALMPLYACIQ	3767
	1280.14	POL	694	95	95	LCQVFADATPTGWGL	3768
	27.0282	POL	750	85	85	SVVLSRKYTSFPWLL	3769
	27.0202	X	13	95	90	RDVLCLRPVGAESRG	3770
	1186.07	X	50	95 95	90	GAHLSLRGLPVCAFS	3771
	1186.29	X	60	95	90	VCAFSSAGPCALRFT	3772
A I a a siala sa	1280.20	ENV	330	100	80	SVRFSWLSLLYPFVQ	3773
Algorithm		NUC	28	85	80	RDLLDTASALYREAL	3774
	1280.19	POL	28 56	90	55	VGNFTGLYSSTVPVF	3775
	1298.02			90 95	75	TNFLLSLGIHLNPNK	3776
	1298.03	POL	571			YPALMPLYACIQSKQ	. 3777
	1298.05	POL	651	95 05	55 60	KQAFTFSPTYKAFLC	3778
	1298.06	POL	664	95 85	60	PLPIHTAELLAACFA	3779
	1280.181	POL	722	85	80		3780
	1280.09	POL	774	90	80	GTSFVYVPSALNPAD PLGFFPDHOLDP	3781
DR3-motif	795.05	ENV	10	0.5	95	· · · · · · · · · · · · · · · · · · ·	
	35.0090	ENV	312	95	90	FLLVLLDYQGMLPVC	3782 3783
	CF-03	NUC	28	85	80	RDLLDTASALYREALESPEH	
	35.0091	POL	18	90	65	AGPLEEELPRLADEG	3784 3785
	35.0092	POL	34	100	85	NRRVAEDLNLGNLNV	3785
	35.0093	POL	96	85	60	VGPLTVNEKRRLKLI	3786
	35.0094	POL	120	100	1,00	TKYLPLDKGIKPYYP	3787
	35.0095	POL	371	100	55	GGVFLVDKNPHNTTE	3788
	35.0096	POL	385	100	45	ESRLVVDFSQFSRGN	3789
	1186.18	POL	422	95	85	NLSWLSLDVSAAFYH	3790
	35.0099	POL	666	95	55	AFTFSPTYKAFLCKQ	3791
	35.0101	X	18	95	35	LRPVGAESRGRPVSG	3792
Lower	799.01	ENV	11	80	75	PLLVLQAGFFLLTRILTIPQ	3793
conservancy	799.02	ENV	31	95		SLDSWWTSLNFLGGTTVCLG GYRWMCERRFIIFLFILLLC	3794
conservato)					75		3795

## Table XXXIII. Candidate HBV-derived HTL epitopes

Selection			_	Conse	rvancy		
criteria	Peptide	Mol	1st Pos	Core	Total	Sequence	SEQ ID NO:
	1298.01	ENV	117	80	40	PQAMQWNSTTFHQTL	3796
	1280.06	ENV	180	80	80	<b>AGFFLLTRILTIPQS</b>	3797
	1280.11	ENV	245	80	80	IFLFILLCLIFLLV	3798
	CF-08	NUC	120		90	VSFGVWIRTPPAYRPPNAPI	3799
	1186.25	NUC	121	95	90	SFGVWIRTPPAYRPP	3800
	1280.15	POL	501	80	80	LHLYSHPIILGFRKI	3801
	1298.04	POL	618	80	45	KQCFRKLPVNRPIDW	3802
•	1298.07	POL	767	80	70	AANWILRGTSFVYVP	3803
	1298.08	POL	827	80	60	PDRVHFASPLHVAWR	3804

Table XXXIV. HLA-DR screening panels

	Avg.	10.4	24.4	14.0	44.6	20.5	•	110	15.1	43.2	•	15.1	CCI	29.4	11.9	8.9	20.4
	Hisp.	10.1	29.8	16.6	51.1	15.0	•	6.7	10.5	30.5		23.3	19.1	39.0	14.4		19.7
Phenotypic Frequencies	Chn.	4.5	21.9	15.0	38.7	22.0		10.0	12.2	48.9	•	10.7	19.4	29.0	7.3	9//-	24.2
Phenotypic	Jpn.	10.7	40.4	1.0	49.3	30.9	<u>.</u>	376	14.6	61.0	٠	25.0	4.9	29.2	0.4	2	13.5
	BIk.	8.4	6.1	11.1	24.5	14.8	2		16.5	33.9		10.9	0.81	27.8	19.5	5.5	24.4
	Cauc.	18.5	23.6	26.2	59.6	100	2	. 76	21.7	42.0		5.5	17.0	22.0	17.7	2.8	20.2
itive Assay	Alias	(DRI)	(DR4w4)	(DR7)		(In cucad)	(DD2m2))	(DRZWZ 112)	(DR6w19)		(DR4w15)	(DR8w2)	(DR5w11)		(DR3w17)	(DR5w12)	
Representative Assay	Allele	DRB1*0101	DRB1*0401	DRB1*0701		105141000	1001 1900	DKB3*0101	DKB1*0901		DRB1*0405	DRB1*0802	DRB1*1101		DRB1*0301	DRB1*1201	
	Alleles	DRB1*0101-03	DRB1*0401-12	DRB1*0701-02		DBB1#1601 03	DKB1*1301-03	DKB3*0101	DKB1*09011,09012		DRB1*0405	DRB1*0801-5	DRB1*1101-05	·	DRB1*0301-2	DRB1*1201-02	
	Antigen	DR1	DR4	DR7	Panel total	cad	DIK2	DR2	DR9	Panel total	DR4	DR8	DRII	Panel total	DR3	DR12	Panel total
Screening	Panel	Primary	•		1	-	Secondary			1	Tertiary	Ì		•	Quartemary		

Table XXXV. HBV-derived cross-reactive HLA-DR binding peptides

			Conse	Conservancy						HLA	DR binding	HLA-DR binding capacity (IC50 nM	C50 nM)					Total DR
Peptide	Mol	1st Pos	Core	Total	Sequence	SEQ ID NO:	DRI	DR2w2 81 DR2w2 82	DR2w2 82	DR3	DR4w4	DR4w4 DR4w15 DR5w11	DR5w11	DR6	DR7	DR8	DR9	alleles bound
F107.03	POL	412	8	8	LQSLTNLLSSNLSWL	3805	2.0	21	0001	≈.	9.4	47	294	135	167	557	682	10
1298.06	Z Z	99	95	8	KQAFTFSPTYKAFLC	3806	9.4	38	143		4	173	83	175	92	408	139	01
1280.06	EN	180	8	8	AGFFLLTRILTIPQS	3807	Ξ	217	1053	•	8.5	253	5.6	9.5	80	88	28	6
1280.09	POL	774	8	08	GTSFVYVPSALNPAD	3808	14	650	400		811	93	426		93	803	221	6
1186.25	NUC	121	95	8	SFGVWIRTPPA YRPP	3809	532	827	47		577	603	692	17500	1042	196	938	~
27.0280	NUC	123	95	8	GVWIRTPPAYRPPNA	3810	14	217	2.8		=	<i>L</i> 9	42		114	35	1991	00
CF-08	NUC	120		S	VSFGVWIRTPPAYRPPNAPI	3811	192		105		300		426		124			٧.
27.0281	POL	145	8	8	RHYLHTLWKAGILYK	3812	17	5.4	35		2250	1462	42	745	61	27	174	00
1186.15	ΕN	339	95	95	LVPFVQWFVGLSPTV	3813	385	13	1429	•	300	23	53	1944	2717	74	8	7
1280.15	M	201	8	8	LHLYSHPIILGFRKI	3814	727	268	200		99	238	488	17500		803	1531	7
F107.04	М	523	95	95	<b>PFLLAQFTSAICSVV</b>	3815	28	337	4762		563	317	1667	44	325	845	1271	7
1298.04	POL	819	8	45	KQCFRKLPVNRPIDW	3816	3.3	4136	952		38	45	1538	814	63	845	3000	7
1298.07	PQ.	191	8	2	AANWILRGTSFVYVP	3817	54	379	3279		882	1520	1429	140	43	196	278	7
857.02	NUC	20		06	<b>PHHTALRQAILCWGELMTLA</b>	3818	2	9.1	211		82		263	193000	9/9	961	2273	7

a. A dash (-) indicates IC50 nM >20,000.

Table XXXVI. HBV-derived DR3-binding peptides

			Conservancy	vancy			
Peptide	Mol	1st Pos	Core	Total	Sequence	SEQ ID NO:	DR3
1280.14*	POL	694	95	95	LCQVFADATPTGWGL	3819	<i>L</i> 9
35.0096	POL	385	100	45	ESRLVVDFSQFSRGN	3820	115
35.0093	POL	96	85	09	VGPLTVNEKRRLKLI	3821	136
1186.27	POL	420	100	85	SSNLSWLSLDVSAAF	3822	200
1186.18		422	95	85	NLSWLSLDVSAAFYH	3823	231

\*tested as peptide 35.0100

Table XXXVIIa: HBV Preferred CTL Epitopes

Peptide	Sequence	SEQ ID NO:	Protein	HLA
924.07	FLPSDFFPSV	3824	core 18	A2
777.03	FLLTRILTI	3825	env 183	A2
927.15	ALMPLYACI	3826	pol 642	A2
1013.01	WLSLLVPFV	3827	env 335	A2
1090.77	YMDDVVLGV	3828	pol 538	A2/A1
1168.02	GLSRYVARL	3829	pol 455	A2
927.11	FLLSLGIHL	3830	pol 562	A2
1069.10	LLPIFFCLWV	3831	env 378	A2
1069.06	LLVPFVQWFV	3832	env 338	A2
1147.16	HTLWKAGILYK	3833	pol 149	A3/A1
1083.01	STLPETTVVRR	3834	core 141	A3
1069.16	NVSIPWTHK	3835	pol 47	A3
1069.20	LVVDFSQFSR	3836	pol 388	A3
1090.10	QAFTFSPTYK	3837	pol 665	A3
1090.11	SAICSVVRR	3838	pol 531	A3
1142.05	KVGNFTGLY	3839	pol 629	A3/A1
1147.05	FPHCLAFSYM	3840	pol 530	B7
988.05	LPSDFFPSV	3841	core 19	B7
1145.04	<b>IPIPSSWAF</b>	3842	env 313	В7
1147.02	HPAAMPHLL	3843	pol 429	В7
26.0570	YPALMPLYACI	3844	pol 640	В7
1147.04	TPARVTGGVF	3845	pol 354	B7
1.0519	DLLDTASALY	3846	core 419	A1
2.0239	LSLDVSAAFY	3847	pol 1000	Al
1039.06	WMMWYWGPSLY	3848	env 359	Al
20.0269	RWMCLRRFII	3849	env 236	A24
20.0136	SWLSLLVPF	3850	env 334	A24
20.0137	SWWTSLNFL	3851	env 197	A24
13.0129	EYLVSFGVWI	3852	core 117	A24
1090.02	AYRPPNAPI	3853	core 131	A24
13.0073	WFHISCLTF	3854	core 102	A24
20.0271	SWPKFAVPNL	3855	pol 392	A24
1069.23	KYTSFPWLL	3856	pol 745	-A24
2.0181	LYSHPIILGF	3857	pol 492	A24

Table XXXVIIb: HBV Preferred HTL epitopes

Selection				Conservancy	vancy		
Criteria	Peptide	Mol	1st Pos	Core	Total	SEQ ID NO:	Sequence
DR supermotif	F107.03	POL	412	96	06	3838	LOSLTNLLSSNLSWL
	1298.06	POL	664	95	. 09	3859	KQAFTFSPTYKAFLC
	1280.06	ENA	180	80	80	3860	AGFFLLTRILTIPQS
	1280.09	POL	774	8	80	3861	GTSFVYVPSALNPAD
	CF-08	CORE	120		96	3862	VSFGVWIRTPPAYRPPNAPI
	27.0281	POL	145	100	100	3863	RHYLHTLWKAGILYK
	1186.15	ENA	339	95	95	3864	LVPFVQWFVGLSPTV
	1280.15	POL	201	80	80	3865	LHLYSHPIILGFRKI
	F107.04	POL	523	95	95	3866	<b>PFLLAQFTSAICSVV</b>
	1298.04	POL	618	80	45	3867	KQCFRKLPVNRPIDW
	1298.07	POL	191	80	70	3868	AANWILRGTSFVYVP
	857.02	CORE	20		06	3869	<b>PHHTALRQAILCWGELMTLA</b>
DR3 motif	1280.14	POL	694	95	95	3870	LCQVFADATPTGWGL
	35.0096	POL	385	100	45	3871	ESRLVVDFSQFSRGN
	35.0093	POL	96	85	09	3872	VGPLTVNEKRRLKLI
	1186.27	POL	420	100	85	3873	SSNLSWLSLDVSAAF